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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the

15 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

20 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

25 As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

30

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.
10
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30
$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

- The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.
- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
- 30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified.

Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a
5 Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next
10 generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.
Optional additional components of the kit include, for
example, restriction enzymes, reverse-transcriptase or
polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and
enzyme substrate and chromogen if the label is biotin), and
the appropriate buffers for reverse transcription, PCR, or
hybridization reactions. Usually, the kit also contains
instructions for carrying out the methods.

10 The following Examples are offered for the purpose of
illustrating the present invention and are not to be
construed to limit the scope of this invention. The
teachings of all references cited herein are hereby
incorporated herein by reference.

15

EXAMPLES

The polymorphisms shown in the Table were identified by
resequencing of target sequences from three to ten
unrelated individuals of diverse ethnic and geographic
backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The
strategy and principles for design and use of such arrays
are generally described in WO 95/11995. The strategy
provides arrays of probes for analysis of target sequences
showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.
The reference sequences were sequence-tagged sites (STSs)
developed in the course of the Human Genome Project (see,
e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154
(1996)). Most STS's ranged from 100 bp to 300 bp in size.

30

A typical probe array used in this analysis has two
groups of four sets of probes that respectively tile both
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence. That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACTCCACTTGAAGCCAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTT
						GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT
						GTA CTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAGCTTTTGAGGATAATGT
WI-7070	226	C	T	---	---	TACTAGACTTTATGCCATGGTGCTTT[C/T]AGTTTAAATGCTGTCTCTGTCTG
						AAGCCATTGACGTAACATCTCAGAGGTTATTGTCATGGATTGACTCCTGGGACAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT
						GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAAGAAACTGAGACAGATAATTCTGAATT
WI-10744	61	G	C	---	---	AAATGAGGTAAGTTTCAGGCATCA
						GGGCAAAATTACAGCAAAAGTCAAAATTACCAGCATCAAAAGTCAGGTGCAAGGAGGTAGAACAA
						TTACAGTAACTATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAAAT[C/T]AGTG
						GGTCCCTAATAGTTATTAGTTCCTTTTCTCCCTCTCTCTCAATCTCTGAAATTTATTTTATACCTAA
WI-9975	126	C	T	---	---	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATTTCTTACTGAA
						GCTAGGTTTTGTTTCTGTGGCTGTCTTCTACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT
						GATGTAAGTGTCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTCATCCTGTATTAAATTTCTTCCCATATTAAATCAAGGGAGTGGACAGGT
WI-8010	247	G	T	---	---	CCCTGGCTGAAAAGAAATAAGAGATCCCAAGTGGTGGG[G/T]CTT
						GCCCGGCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTTCTCCATCCTAGGATTCGCCCTATAAT
						CTTTGTCCCTGTCTGT[G/C]ATTACCTGATTCTACTTTTGTATACACAAGGCTGATGGCTCACAAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G	C	---	---	TCTCGACTCTATAACAACCTCCAACAGAA
						GCCCGGCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTTCTCCATCCTA[G/C]GATTCTGCCCTAT
						AATCTTTGTCTGTCTGTAGATTACCTGATTCTACTTTTGTATACACAAGGCTGATGGCTCACAAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G	C	---	---	TCTCGACTCTATAACAACCTCCAACAGAA
						TATGCACCTCCACAAAAGCGATATAATTTAAAGTTTTTTTTCATTAGAAATAAATGTATAAAATAA
						ATATGTTATTATAGGCATTTATTACTAACTATAGTCTTCTTGGAAAGGAACACCCAAACCAATACTT
						ATAAGTACATGTAAATTTATAGTAACATAATTTTACTATATACATAATGGAATAATCATATTCTCACA
WI-8007	242	C	A	---	---	GAAGAGCTGAACAGACATTCACCGGATACGACTGTGGAC[C/A]AGCTGCTG
						TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTGTAG
						TCTATATTCACACATATGAGTGAAATTTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACTATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTTAC
WI-9823	97	C	T	---	---	ATGCTTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTCTACATTCTATGGACAACTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCTCT ACTTGTCTCATGTACAAATTTTCTGCTCGTCTTCA/ATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTTATAGGCCTCTG TCTTTAAACCTGTAATGGTATATTAAATCCTTGGTGTTTGAATGTCCTC
WI-9651	139 T C ---	---	TCTCTACATTCTATGGACAACTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCTCT ACTTGTCTCATGTACAAATTTTCTGCTCGTCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CT/CJACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTAATGGTATATTAAATCCTTGGTGTTTGAATGTCCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGTCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGTCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTTCTCTTGGTGCTGCTGGTTCAGGGGCGAGGAAGCGTGTGGACTGCAGCTTCTGTCTGTGC TCCCCCGTCTCCTGGAGGCGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGTCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGTCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/CJGGCTTCTCTTGGTGCTGCTGGTTCAGGGGCGAGGAAGCGTGTGGACTGCAGCTTCTGTCTG GTCTCCCCCGTCTCCTGGAGGCGAGTATAGGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGTCTGGTCTGTTCAATTCACCTTCTCTCTCCTCCATGAAGAGGATAATTAAGCATCATTT CATCTGGCCCTTTTGTGATTTTGAATATTTTGTG/JG/JTGACTCCTATGCACATGATAAATTTGTTA TGCTTGTCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTTATGAGGAGAAAAGGGA TCACCCCTTTTGTCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATATAGGGAAAATAAGACAATTTGAA/T/A,CJGTACCCCGAGAAACAAGAG CCCTGCACCTGACTCCAAAAGGAGTTCTATTATCTGGCTGTTTCCAGACTTTATTGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCCACTCCCCTCATCAGGCCAAAGTGGAGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTTGCATGCGCTCTATTCCCTCTGCTCTC/CJ/CCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---	---	ATAAACCCCTTGTGTATGTATCACCCAACTCACTAATTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCAGCTTATTTTGAAGAAAATCCTAAACATCAATACCTTTCATCCATAAAATGTCAGCATTT /CJATTAATAAACAAATAACTTTTAAAGAAACATAAGGACACATTTTCAAATTAATAAAATAAAG GCATTTTAAGGATGGCCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132	A C ---	---	TCTTATTGCATTTACAGTAGCCCATGAAGTAGGTAAACCAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAAGCAAAGACCTGCAI/C JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCCAG
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCTTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAAACTTTGTGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGTAATTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCAATTGAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T ---	---	AAACACACAGATCATCAAGCAC[A/T]ATCTGTGTGTTGAGATAAATGATGCTGAGTCACCTATG TAAGAACTAATCTGAAATAGTAGGATAGTATTATCATTTCTGTATAGATTACCTCTCAGCAAT TGGTCTGTTTCACTTATGGAACCTCTCCGTACTGTAAATTTTCACTTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGCC TTTCAATAAAAGAGTACATGATTGAACATGTGTTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGTTGGGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTT[G/J]ACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATTTCTGCTATGCTTCTCAGATTGCAGAAAAATCAG TGCTCAAAATTCCTTGTCACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70	G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGTTGGGTGAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTTACGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATTTCTGCTATGCTTCTCAGATTGCAGAAAAATCAG TGCTCAAAATTCCTTGTCACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACAGCCTTTTATTGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGAATGGGTGGGGTGTACCCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGGAGAGGGAGGCCAGACAGGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACCTTCT[G/C]ACTGCAGAGTATAGGGACCGGTTCCAACTTT
WI-9484	178	G A ---	---	TCAACAGCCTTTTATTGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGAATGGGTGGGGTGTACCCTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGGAGAGGGAGGCCAGACAGGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACCTTCTGACTGCAGAGTATAGGGACCGGTTCCAACTTT

WI-7330	207 C T ---	---	---	AGGATGGAAGGAGACACGGGGCAGGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211 G A ---	---	---	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAGGGATGTGATTACAATTTAATGAATCAGTCACCT GCACAATTATCCTCTTGGCATCATACAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCATGCCACTT
WI-7166	59 C T ---	---	---	TCTCTCAAAAGAGAAAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGTTTAACTTGTGTTGCTGTGAACAATTGTCGAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTGTTAGATTCAAGGCCCGAG
WI-7259b	189 T C ---	---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCCCTCTGGCT GGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCCTAACCTGGCCACAG[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTGCAGGGGCCCACTTCCCCTGGAGCTC
WI-7259	188 G T ---	C	---	GCTTCTCCOCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCCCTCTGGCT GGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCCTAACCTGGCCACA[G/C,T]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTGCAGGGGCCCACTTCCCCTGGAGC
WI-7322	275 A G ---	---	---	GTACTTTAGGCTGTGGAGGTGGGCAATTTAGTGGTGACCTTGCAACAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAACTGCCCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCCCTTGTACATAGAGAGTTTGTATGGGGCTCTGGCTG
WI-7685	46 T C ---	---	---	TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCTC[C/T]TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAAGGTCTTGGAGCTGAGCCTCTCACCTGTACTCTCCGAAAATCCT CTTCCCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCCTCCCTCCTGCCGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTTCTGTCTC
WI-563	87 G A ---	---	---	TGTGACCAATTGTTATTTAGAGGGTTTAAACAATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGAGGGCCTCCCT[G/A]CCCTGATCATGTCTACCTAACTGCCTACTCTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCAGAT

WI-931c	191	C A ---	---	GACCAGGCACGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCACTTACTGTTGATGGATTATAATTATTGTCCAAAAGCC[C/A]JGAGCCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G ---	---	GACCAGGCACGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]JTCCTCACCACACCTTCCAGTGCTTATTCTGCTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTTGATGGATTATAATTATTGTCCAAAAGCCCGGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G ---	---	GACCAGGCACGAAAGCCACGGAAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATTCTGCTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTTGATGGATTATAATTATTGTCCAAAAGCCCGGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCAATTTAATAACGTTGCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGGACCTACTTAG[A/G]ACAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCAATTTAATAACGTTGCCCCCC
WI-7719b	281	T C ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCAGTATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCAGTATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCCTCCACTTTCATTTTCTTGAAACATTGCTATCAACTGGGAA GAGT[C/A]JGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTTA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGGTGCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	TCCCTTTATGACCCAGAGATATTTAATACACCAATTACGTAGCAGGCCATGGCTCATGGACC CACCCCGTGGCACTCATGGAGGGG[C/G]TGCAGGTGGAACTATGCAGTGTCTCCGGCCACACA TCCTGCTGGGCCCCCTACCTGCCCAATTCATCTGCCAATAATCCTGCTCTTATTTGTTTCATCCTG GAGAATTGAAGGGAGGTCAGGTTGTTGTCAATGATTTGTCAGAGAACCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGGAGCCGCCACCAGATGCTGAATCCCCATCCCATTCGTC[G]GATGAG TCCCATTTGCCCTTGCAATTAGCATTCTGTCTCCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCCGGGCAGGTGCAGCCCTTCCTCC TGTCCTGC[C/G]CTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGTGCTCCCTCTG TGTCGCTCTCATCCATTCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGATTCT CAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCCTACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTTCATAAAGATT CCTCAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	ATTGCACGTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGT ACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAAGGAAGGAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	ATTGCACGTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	ATTGCACGTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAACTGTGTTGAAACAGAAATAAAGTC AAAGGAACAATAATTACAAGAACCATGCAGGAAGGAAACTATGTATTAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAACTGTGTTGAAACAGAAATAAAGTCAAA AGGAACAATAATTACAAGAACCATGCAGGAAGGAAACTATGTATTAAT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGC[A/C, T]GTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAACTGTGTTGAAACAGAAATAAAG TCAAAAGGAACAATAATTACAAGAACCATGCAGGAAGGAAACTATGTATTA
WI-7227d	99 G C ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTATCTTTTCCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTATCTTTTCCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTATCTTTTCCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCAGGCATCATTAACAAGCCAGTAGGTCACCTGGC TTCCGTGGACCAATTATCTTTTCCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCACAATGCCCTCTCCACGATGTCAAGGACTCCTGTCTGCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAACTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAACAGGCTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCTGCCCTCCCA[A/C]ATGATCTTGAGATTTC

WI-7310a	64	T A ---	---	CCACAATGCCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGAGACAAGGAACQI/A JCCGAAGAGGAAGCAAGAACCGTACTGTCTATGTTGTGATCCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACAGGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162	A G ---	---	CCAGCAACACCTACACCCCTTGTCACCTGCCCTGGACTCCTATGATGGCCTGCTGTTGATAATAATCA GATCATGCCCAAGACGGCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG[A/G]GTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTCACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51	C G ---	---	CCAGCAACACCTACACCCCTTGTCACCTGCCCTGGACTCCTATGATGGCCTG[C/G]JGGTTGATAATAA TCAGATCATGCCCAAGACGGCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTCACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213	C T ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGTTGAGATC AGATGTGGCCCAAGGGAAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGACA AAAGGCCCT[C/G]JGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C G ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCC[C/G]CTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGTTGAG ATCAGATGTGGCCCAAGGGAAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C G ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGTTGAG ATCAGATGTGGCCCAAGGGAAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G A ---	---	AAATTGCTCTATTCCGGACCCCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAA[G/A]GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAATAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92	G A ---	---	AAATTGCTCTATTCCGGACCCCTCATATTAAATAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAA[G/A]GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAATAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGTTC[C] GTCTACCATTTTACCAAAATTCGTTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-1795a	47 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT[C]CTTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGTCTTGCAGAAAGAAAGTC GTCTACCATTTTACCAAAATTCGTTAGTACAAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-10616d	136 G A ---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCTCCATACGTAGTCTCTGGTCTCTATCACAATTGCCA C[G/A]TAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136 G A ---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCTCCATACGTAGTCTCTGGTCTCTATCACAATTGCCA C[G/A]TAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141 C T ---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCTCCATACGTAGTCTCTGGTCTCTATCACAATTGCCA CGTAGC[C/T]CTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116 G C ---	---	CACACAATTTGCAACACTTCAAGTGAAGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGCTCTCTCCATACGTAGTCTG[C/C]CTCTCTATCACAATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52 G A ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACT[G/A]ATACTAATAAA AAACCCCTGTAAAGTCTGCTTGCAATTTTCAAGATTCAATATATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATATTTAATTTCAAGTTTCTCAAAAGGAATATGAAATTT TGTTAAATGCAATCCAGCTGTAACTTTTGGACTTGTCTTTATTTCTT
WI-1126b	230 T C ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAAAAA CCCTGTAAAGTCTGCTTGCAATTTTCAAGATTCAATATATATATCCAGATTGTTTCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATATTTAATTTCAAGTTTCTCAAAAGGAATATGAAATTTGTT AAAATGCAAAATCCAGCTGTAACTTTT[C]GGACTTGTCTTTATTTCTT

WI-1126a	97 T C ---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGGCAAACTCCAGTATCACTGATACTAATAAAAA CCCTGTAGTCTGCTTGCATTTCAAGATTC/CJCAATATATATCCAGATTTTCCAGCAAGAA ATTTTATTCTCAAGATATAAAAAATAAATATTTAATTTTCAAGTTCCCTCAAGGAATATGAATTT GTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGTCTTTATTTCTT
WI-11183c	124 C T ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTATGACATACAAATGACCACAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCACAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAAATTCAGATGATTTTGGCCCTTGTCACATAACAT TTTATGACATACAAATGACCACAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTTGGCTTATAGTCTTATGCTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCAATTTCCCTCTATCTGGAGCGCTCTTCCCTGTACTTTCTCIG TTCACCAACCTTCTTTTATTTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTCTCC
WI-10770a	49 G T ---			GCTTGGTTTGGCTTATAGTCTTATGCTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTGTATT TCACCCATACCTCTATGCCCTGCTCAGACCAATTTCCCTCTATCTGGAGCGCTCTTCCCTGTACTTTCTC CTGTTCAACCAACCTTCTTTTATTTCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTCTCC
WI-9667b	82 C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCGAGCGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGTTATTACACACAGTATAGGCATGGTACACTAATGGATCTTGGCT GTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCATTCT
WI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATG G/CJTATCACTGGACACAGCCACCTCCCGAGCGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGTTATTACACACAGTATAGGCATGGTACACTAATGGATCTTGGCT GTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCATTCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACAATATTTTATTCTAATTTT TCCTTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCACTTACTTGCAAATTATTCAAAGCGTTAATGCATTATG
WI-10400c	166 A C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACAATATTTTATTCTAATTTT TCCTTCCCTTACCTTTACTCCTCCCAACCA[A/C]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCACTTACTTGCAAATTATTCAAAGCGTTAATGCATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACAATATTTTATTCTAATTTT TCCTTCCCTTACCTTTACTCCTCCCAACCA[A/G]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCACTTACTTGCAAATTATTCAAAGCGTTAATGCATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCACTTACTTGCAAATTATTCAAAGCGTTAATGCATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAACTAAGGCCAAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTCACCA[C/T]TTAGAAAAGGGCATTTCAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAACTAAGGCCAAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGAG CCCCACCTCTCACCACTTAGAAAAGGGCATTTCAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	CGAGCTTGGGATAAGCAAGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACTAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAAGAACTGTGAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	ATACGCTTTCTGTCTGCCACAGTGGAAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCTTCAGCTTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	ATACGCTTTCTGTCTGCCACAGTGGAAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACA[C/T]AG CCCTCAGCCCTTCAGCTTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAAGTGAGTGACGGTACCT GTGAGCCCCCATCTCT[G/A]TGGGATAAAGGTGTCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGAT[A/T]AAGAAGTGAGTGACGGTGA CCTGTGAGCCCCCATCTCTGTGGGATAAAGGTGTCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAA[A/T]GGATAAAGAAGTGAGTGACGGTGA CCTGTGAGCCCCCATCTCTGTGGGATAAAGGTGTCCATTTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCTGAAT TTCATATACCTCCATTATTAAATTCATATCATCATTCAGAGAGAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGTAATCTCTAAA
WI-6711a	36	T C	---	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAAT[C/G]TAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCT GAATTCATATACCTCCATTATTAAATTCATATCATTCAGAGAGAAAGACAAACGGTGCCCAACTG GGTTGGTGGTGCCTGCACACCCACAGTGGCAACTAAGTGTAATCTCTAAA

WI-10613b	172	A C ---	---	ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAATTTATTTCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGCAACTTTTGACAAAGGCCAGGCAATTTTATTTG[A/C]GCCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A ---	---	ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACA[G/A]TGTAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAATTTATTTCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAAACAAAGTGACTACCCTTGAAGC ACATCCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCCTGAGGAA[A/V T]GGAATGAACCACCTCCCTGCCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAAACAAAGTGACTACCCTTGAAGC ACATCCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCCTGAGGAA AGGAATGAACCACCTCCCTGCCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCC[C/T]GAAGATCTGTGCTTTCCAAACAAAGTGACTACCCTTGA AGCACATCCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCCCTGAGGAA AGGAATGAACCACCTCCCTGCCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103	T A ---	---	ATGACTCAGGTGACAAAGAAAGCATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAC ACAGAAAGCTAAAGACATCCCTTTTAAAGAGCC[T/A]AAAGACAGCCATTTTAACTCCTAATTG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-10681a	41	A T ---	---	ATGACTCAGGTGACAAAGAAAGCATGTCCTAGACCCCATTTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAGCTAAAGACATCCCTTTTAAAGAGCCCTAAAGACAGCCATTTTAACTCCTAATTG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-7222c	126	G T ---	---	GCCTCTCCTCAACTGTCCTGGACCCCAAGGCTAGGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATCCCTTGAACAAGAAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	---	GCCTCTCCTCAACTGTCTCTGGACCCAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGTCCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCCTCAACTGTCTCTGGACCCAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGTCCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTT[C/A]TTATCTCTCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCCAACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCCAACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGTACAGA[G/TAATCCTTGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCCAACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCCAACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAACCTTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGGAAGTTGAAACACGAGACGATAGTTAACGCTGTTAAGTTTAT ACGGTGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTCTTTGTG TTTTAGACACAGGCTGCTGTGTG
WI-10854a	102	C T ---	---	---	TTCCACAAAACCTTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGCTGTTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTCTTTGTG TTTTAGACACAGGCTGCTGTGTG

WI-9826b	127	G A ---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCCGTGATGGCTGTTGGTGTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT CAAGCCCAAAAAAAATTTACTCTCTGGCCCTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GGCAGAGAAGATCAGAAAGTGTGAA
WI-9826	125	A T ---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCCGTGATGGCTGTTGGTGTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTTATTTGGCCCTTC AAAGCCAAAAAAATTTACTCTCTGGCCCTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAAGTGTGAA
WI-15986	60	T G GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTTTT[G/J]TAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	CCACCTGGGGC TCCC	TTCAAGTAAGTCAAAATAGGAAACAGAG[A/G]GGGAGCCCCAGGTGGGACAAATCATGGCTACCCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCCCTACACCCCTTTAT
WI-8170b	259	G A ---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTTCTCTACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA ATAAGGTAAAAGGCCCTCAAAATGAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTTCTCTACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAAGGCCCTCAAAATGAATCTACGGAAAAACATAACAC
WI-8172	136	C G GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTATTAAATTTCTTCTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTCTCACCCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	AGCAGGGTTTGAAATTGATCCCTTATTTACATGAAATAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	GCCTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCCAAGCATGGGATTTTGCCCGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCTG TTCTTAACCAGCAGAGCCCCAGCAACCTAGAAAGCCCTCACCTAGCCTCTTAAT

WI-8827	22	C T	TCCCTGGGAG ACTATGG	GGGATTAGGAT TTTAGTGTTCAC C	GGTGCCCTGGGAGACTATGG[C]/TAGTGAACACTAAATCCTAATCGCCATGCATTGGAAATTATT CCGACTATTACTTTCTTTAGTTCCTTCTTATCCACCCAGTCTCT
WI-8833	51	A T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCGGCCCTCTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A]/TGGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63	A G	---	---	ATTTTAGCCATGTTGGTAAAGTTTCATTTTCAGTACATGGGTAAACACCCAGGCCCTTTCCC[A/G]T TATATCCAGGTATGCTACAAGTTCTTTTAACTCTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCCTCATTATTTTATCCTGAAGCTCGTG
WI-8850	21	A G	GGGACTTAAC CTTTGGCCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCCTGGCTGTTTGGCTCTCGCTTGCTGTTTTTGGTTCTT TCTCTTCTACTGGTCTTTCTTTGTCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79	C T	CCCGGGCATTG AGGATA	AGTCTTCCCTGA GCCTTCCAT	ACTTTTCTTGAGCTGAGCAACCTCATCTCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACA[A/G]ACAACATGCT TCGGACTTACCAGGAGAGTGGAGCTTTCCATATAA
WI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAACAACATGCT TCGGACTTACCAGGAGAGTGGAGCTTTCCATATAA
WI-8895	32	A C	---	---	GTCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGATGCTCCAATCGCTCTTTC
WI-8456	93	G C	---	---	CCTTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTGTGAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTGCTCAGTCACTCCAC
WI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTGTGTATCAGTGCATATTTCTATGAAA ATTATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTGTGTATCAGTGCATATTTCTATGG AAATTCATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT TGTGGCCAAGTGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCTCCTGCCGTTGTCCACCATCCACAGAGCA GCCCTAGTGCCAGGTGCAGCCACTGCCACCCACGGCACACGGGAACAGGACCATGCTGC

WI-12108	40	C T	TGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[C/T]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29	G A	CCACAAAGGT CACAGGCA	GGTATAACAG AACCGTATGTA OG	CAGGCAAAACGTCCACAAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCCTCCATCTTTTCTTGGTGAGGACACC
WI-12201	61	C T	CCCACTGATCA CCTGTCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTTCCTGGAGTGTATGTCCCAAGCCCACCTGATCACCTGCATG[C/T]GCCA GGTATGGTGGGGGTGTGATGGACGTGGGTTTGCAGCCCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A T	GGCAGCCAGC TCTGACTT	GGAGAGTGAC AGAAACAGAG AG	TTTTTATCTGTGAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCTCTCTCCCCACATACCA ACTTCTTCACCATGATGATTATACCAATAATACAGTTCCCTTATATGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G	TGGCCTCGCTG CCTC	AGGGATCAA GAGAAAAGGC	TTTTTCGTTTGTATATGATCCGAATGCTTGAGAAGAAACCCTGGCCTCGCTGCCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGGG
WI-15407	92	A G	CATGCCCTTTA AGGATTAAGT TT	TCCTTTCTCTTT TGGTAGTGIGG	AGCATGTAAGGAGCAGTTTTATTGTTGTTATTCAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[A/G]CCACACTACCAAAAAGAGAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C	GTTGAGTATTT GTTCTGCTCAT AATT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGCTAGACATGGCTACACTTTA TACTTTGTGCAATTTAGTTGAGTATTGTTCTGCTCATAATTT[C/C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC[G/A]CTTCCAGAAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCAATTTCAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAAATTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGGAACAGTTGGAAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T	CAGACACAGC ATCACACCA	GACCCCTCCGT GGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAGTACCCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCACGGGAGGGTCCGGGAGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAATTTTTTAA[A/G]AAGGTTTAGCTATTTCCCAATGCTATTTAATACAAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGTTACTGGAGCCCCG
WI-11324	40	C G	GGATAAATCA TGTCGCCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTAICTGTTCTTGTC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAAGGAGAGAGAGTCACTACATAAGCACAGCACATAGTGGAA AGTCGCTAAGTGCTCTACGAGAGTCAATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCAATTTGCAATCACTGTGAAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCAAGTCGTCGCTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA	CTTAAGCATTATAGTTTGGCCTGATGGTGGACACAGAGACTTTCATATTCTTGTTTTAAAGTC TCTTCAGTCAGGAAAGCTACAGATTTAAATAATATGACCATGACTAGATAGAAATCAGC
WI-11388	88	C A AAGTTC	TGTTTGAAATT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGCCAGTTAGCTCAGTTGGTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTCATATAATTTAACTTGGATACAAAGGCATTGTTATGCTAAT
WI-11392	55	T G ATAAATAC	GGTATGTGT CTTGAACCTTA	GTACATTCACG TGTTTTGTAAA	TTCTATCATTCATTAAATGGCAGGTTATGTGTTCTTGAACCTTTAATAAATACCTGCTTTTACA AAACAGTGAATGTACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACGTG CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAATAAGATGGCAATTTGTTTCAAGTTAATTTTGTGAAATGGTGTCTTATGATGGGTGAATA TGAAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A CAGC	TCCCCACCAAC T	TGCCAGGGCCT TATTG	CTGTGAGTCTTCCCACCTAAACCGTGAGTTCAGTATGTCTGGCAGCAGTCTGTCTTGTCTTGGTG TATTCCTTACTGAATCCCCACCAACAGCCTCA/CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T TTTATTTTGCA	TGAGAAGCCA T	GTTTATTGTTA TAAAAATGAC	ACTTGAGAAGCCATTTATTTTGCAGCTCTTCCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGTCAATTTTATAACAATAAACTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTGTAGTAGAGCAGTGGAAACAGTGTGCAATACTACTACCTTCTGTGG TCCCCGTGTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G AGCAGAC	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GOOGGIG	AGGCAACACTGCTTTATTAGGCCGGCAGCCAGGAGCAGACAGTCAACCGGCTCCTCAGTACACATT CCCCACCCCTGCCCTCGGTGCTCCCCACTCAGGGCTGGCATGGAGGGGCGAGCGTAGTCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACCTTAATAATTGCACTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCATAGGGAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACCGGTACAAAATTACA GGTGGTTAGTTCATTACATGAGTACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGAT GGAAGACAC	AACATAACCA CCTGTAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTTGGCTATAGTCAAGTGGTTCTAAACTTGAGCTTGCAAGAGAACACTTGTTGGGCTT[A] GTTCAAACATGGACTGATAGTCCACCCCCAGATTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAAGTTTTTCAGAAAAAATAAAATGACAAGAAC CATA[C/A]AAATATTGAAATTTATTTCATTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46	G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTTAAATAT GTTTGGTCTT AAA	TTTGAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGACCCAAAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAAAATTTCCAGAAAGGCAATTTTCTTTAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAACGTTTCCGGGAAACCTTG GATT[C/T]CCAAGACCCGAAGACTCTCTCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTGTTATTTTGAAGAGTTTGTCTATCTAAATTTTCATATTTTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTCCCTC
WI-11585	79	T C	TGGTTTGCAA AAACAAA	CCATGCTTCAC TGATACTTC	TTAGAAAGGAAAGAAATAAACACACGGTAATGGGAAATCAGTTTCAAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAAAT[C/G]GAAGTATCAGTGAAGCATGGCTAGAAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	---	---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/C]AGAACTAGGGACTTTTCCATGAAAATAATTAGAGCTAAGGAATTTCTGACGCTCACCATTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAA[C/A]ATATTAAAGTATTCTGTCAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAAGTATTCTGTCAGCTAC GGACTTCGT
WI-11626b	83	T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTTTAAAAAAT[C/T]ACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAATTTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAAATTACTTAATAAAGAAATTAGCCATACCACATTGTTCATTGCTAC AAGAACAATTGGCAATGA
WI-11627	23	T C	CCITTCCTTCC ATTGTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTTCCATTGTCCTC[T/C]CTTGAGATGGTTGCAAAATGGGAAGTAAAAAGCAAAAAGGG AGATGAGAAATACCTGATGCCCTTTTGTCTGGCTTACTTCCATTCCGATGTCAAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA TCCT	AGAAACTTGGT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATAATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA CT	GACCCAGCAA AAAGAAATGAT T	GTACCATTCTTATGGTGGCAAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTACGAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAACTGC A A A	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAAGTCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCCTGCAGTTGTTT AAAATGICCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T C	---	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT[C/TT]GCATAAA GGCTGGGAAGGTGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACTTTTGACATCTTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTA ATGCCCAACCATCTTGTGTTTTCAGAATCTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACCT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATACTGAAATAACCCACAGC AG[C/T]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAAACACTGCTAATTTTTTGTCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTTCT	ATCACCAAAG AACAAATTCCA	TGCTGATTCACTGCTTCTACCATCTGGCTGGAATTTTCTCTTCTGTACAAATTTATTG[C/T]GGCTG GAATTTGTTCTTTGGTGATTGTCCCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTTCAAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGCT[A/G]TCCCCGTAAATTTAGAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTCCAGCACACAGCCAGCCACACTCTAGACACGCCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAC[C/A]CTCCTCCCTCCTCCACACACTCCTC

WI-11715b	123	C T	AGCTGGCTGC AGCTT	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49	A C A A A	GCACACAATG TAAACAGAC A A A A	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAA/CJTGCATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTACGCCAC AGGATGGGACTGGGAAGA
WI-11727	43	G C T C A A C A	AACAATCCTT AAAACAATA TCAACA	CCTGIGGTTTG TGTTGCAG	CTGGATTCCTATACCTAACTCCTTAAACAACCTATCAACA[G/C]CTGCAACACAAACCACAGGC AAAATGAAAACAGATGCCCCAGACAGACCCACCACATGGCACACAC
WI-11728	16	C G ---	ATCTGTGGTTT TCGCCCTG	---	TTTTATTATCAAACT[C/G]CAATTCCATTTTCAAAATGTAAATTATCATCAGCTCCCCATCCACTTT CTCCATCTTCTATCTCTTCCCACTTCTCTCCCTACACTTCTCTCCCTACAAACCCGGTTCCAAA
WI-11758	61	A G	ATCTGTGGTTT TCGCCCTG	TGATTGGCCCT GTGGTCTA	TTTTCTCTTTTAAAGTCGCTATACCTAAGAGGAGAACTGTGGTTTTCGCCTG[A/G]TAG ACCACAGGGCCCAATCACACAGCTTCTGTAGAGAACATGGAGAGTGCCCAAGATCACCATCA
WI-11295	37	A G A A T A T A A	GCCTCACAAA GTATTTTCTAA A A T A T A A	AAAAGTGCTCA TCTGTGAATC T	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT[A/G]TAGAGTTACAGATGAGCACTTTTCA CATTAGGTATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTT
WI-11773	93	T C ---	GGCTCAGAGA GCAAGGGAA	AAAACCTCAGA CTGTAATTTT ---	AGCATGATATCTGCCTGGAGTTTCTGTAGCTCAGCAACAGCAGAGTCAGAGATTAGAAATT ATTTATTGCCCTCCTTTTTCCTTCCCTT[C/G]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC CATGACAACTCTTTTATTAAATGGGCTCAGAGAGCAAGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGCGCAGAGACCCCTCTCCACCTTTTCATGCCTGTGTACACACACACTGTCCAAGCCTC AGA
WI-11282	42	C G	CCCACTTACC AAACCCTCTG	CGTAGGCGAG GCTAAGC	TAATCACCCAACTTACCAACCTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTTACAATGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACITTT ATAAAA	TTTTAATCCCAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCCTA
WI-12469b	91	C T A A G T T T A A A	GTTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTCCATTTCTCCCTTTTATAGTTTTTAAATGTTGTTATAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA[C/T]TTGACAGCACAGTTCTTCAAAAGTTTGCTATAGACAAATCTGA AAATTGGTTCTGAAC
WI-11906	52	A G A T C T G A A	TGTTATAACAT CAAAGAAAAGA A T C T G A A	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT[A/G]TGAGGAACTG CAGAAATTAAACTTTCAGTCTAATTTCTCAGAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78	A G	TTTGTGTTGGG		CCTCCTCTGAG	GCAGTTCTCTGAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTTG
			TGGTCAAG	AG	ATTTTCTGAAT	GGTGGTCAAG[A/G]CTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG
						GACTGGCTTGCAAGAGTC
WI-11806	60	T G	CATGAAGAGT		TCCTGTAAAGC	AAAAATACCAATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT
			GGGCAGTTCA	ACTAATAA	CAATTTTATAT	TTATTAGTATATAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C A		---		CCCTAGTGAATACAAACCTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACCTTCCTTAGGCTGAG
						CTCTCTTGGGAATCTAAGATAAAAGAACTGAGATCCTGGGAAGAGGAA
			TGAAGATCAG			
WI-11965	65	T G	ATCTCTGGTTT		CAGCTGTGGTG	ACAAAATTCACAAAGTACACACTGCTTATTTTCTTGTGTTGAAGATCAGATCTCTGGTTTATTTAA[T/
			ATT	AATGTTGAT	AATGTTGAT	GIATCAACATTCACCACAGCTGAAGGAAATTAACCTGAACCT
			TGCCCTACTAC	TGAGGAAATGT		ACCTATTTTGAAACTGCAGAAAGGGCAGGACAAACAAATCACTTCATAGATTTTCTGGGAAATAT
WI-11027	90	T A A	GCTTTTAAAA	GTTACAGTATT		TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAACTGTAAACACATTTCTCTCATTTCTTTACGA
				TTTATT		ATACTTTCTTTTIGATATTGCAAAATTTCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
						TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGTTCAAAAATAATTAAGGATCTTTGTACCTTT
WI-11049	95	C T		---		GTGTTTATTTTCTGTTTCAACTAAGGA[C/T]JAGACTTCAGAAAGGCATAGCTTCCCTTGTAACGTTTTT
						AAACATCTTTTTCATTTGTAGGAAGGAACATTTTCAAAAGCCCAA
WI-15488	69	C T	CCAGATATCA	TAAC		CAACATTTATCAACATGGTAGGAAAAGTTCTCAGCTCTGCACATATAAAAGGACAGCCAGATATCA
			AC			AC[C/T]GTTACAGAAATGAATAAGATGGAAAATTTTAAACAAATTG
			AACAGTTAAT			
WI-13654	49	A G	GAAACACATC		GGCTGGTGAA	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA[A/G]GTATGACATCATTT
			CGT	TGATGTCAT		CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135	C T		---		ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATTTCTGCTT
						TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA
WI-11070a	110	G T	GCCAGCTATCT	CTCTGCACC		GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGAA
						AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGGAGGGCTGATGTTACCTCTAGCGGCGAAACC
WI-12020	121	T C		---		AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC
						ACGTTCTTTGTTCTCCTC

WI-11076b	142	G A ---				CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTTCTTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	AAGGGGAGC	TCCTGCTCTGG	GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCATCGGCTTATCTTCTTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTCTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	CGCAGAAAA	AATTAGTATGG	GGTTATTCAAA	ACCTTTAAAGTTTCTCCCACTCTCCCGCAGAAAAAGGCATATTCAAT[C/J]GTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-14267	28	T C ---				AATTATTGCTGAAATTAGGAAGGGAGCAT[C/J]GAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTCTTCCAAGTATAAAACTCGTA
WI-13892	50	G A TAGAAC	CTTTTCATTTT	TGATGATGTCA	TATACTAAAA	GATTTGTTTATTTCATCTCGCTTTTCTATTTTGCCTTTTAAATAGAACAA[G/A]CTTTGATTTTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-15288	108	C G TTCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT	TCCCTTGA	ACCTCTTTCTGATGACACTTGACCTGTACCTGTAAAGGGTCTAGAGAGAAAGTAGTAGCTCTACTTTGC TACAATTTCAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[C/J]TCCAAAGGAAAGCTTTTGGC
WI-13951b	88	G C ---				AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAATAATTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C T CAAAA	GGAGTGAACA	TTCTCTGATC	TGGGGTCT	AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAAC[C/J]AGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAATAATTACTGAACACTTGCTATGTGCTG G
WI-13264	25	G A TTGCCCAT	AAAAAGGCTC	GGAGGGAGAG	ACGGAATA	GAGACCAAAAAGGCTCTTGCCCAT[G/A]ATTCCCGTCTCTCCCTCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCATGGCATGGTGATGCCCTCTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
WI-13960	39	A C TGATAGA	AGCAAAAGGA	CATGAAAGGA	C	TTATTGTCTATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTCATGCA TTTGTGGAGCAAGTACTAATTGTTCACTGTCTTTCCCTCACAAGGAGTTGAGCCCTTAGATGAC
WI-15843	62	C T CAG	ATCTTATAACC	CTCTGGCTCAG	ACTTGCCT	AACTCTTTATTGTTAGCTAGCCCCAGTGACTTTTATGCATCTTATAACCAAGAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTTGCTCAGGGTCCACAGGAACCCAGGCTTGGCT

WI-13983	52	G A	TCCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCAGTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACCTCACTGACTTACAGAAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAGAAATAAATAAGATGGACTTGCAGGTGTAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGAACCTGCCATCATCACAGAAAGGCCCGGAAATATGAGTGAGACTCA
WI-14284	55	C T ---	---	---	ATTTCAAACAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGAAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCCTTCC ACCAAATCTT	ATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTGGTGAGGGGATA CCGCTGCTATCCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T ACAAC	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCACTAATAACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGAAATTTTGCAGAGAAATAATA
WI-13529	42	T C TTACCA	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCATTCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCTCGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A ---	---	---	TTATTTGTCAGAAATTTCCAGAATCAGAGTCTCTACTGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAAGTCAAGGAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGAGAAAT TAAGCACCAAGCTTCCAGTTGTCTCTCCAGTCCCATTAACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTTCATTAGCTTGCTTCAAAG[G/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAAATTAAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAGG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTTCATTAGCTTGCTTCAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAAATTAAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86	A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAG[AT]AAATGTTTCTGAAATGTGCACACTAGAAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89	T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAAGAAATCAACA TGTGCACAAAAGAGTAAAAT[T/G]ACCAAAAAATTAAGATTTTTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43	C A AGACTGGGA	TGCAATCTAG	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCTAACTGCGCAGAG AAATCAAAAGACCGATGGTGTGAAATCTGGGCAGCTTCAAAATTTCTGCCTCCTAAAACATTTTCAC CCAATTTTTCATTATTGCC
WI-13857	28	A G ---		---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCATTTTGTGTAGCTTTCATACAGTACAGATTTTCATTGATGTGCTGCCACATCTG
WI-15809	77	T G TGTAATGCC	TGGTTTCTGT	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[T/G]TTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123	A T ---		---	TAAATCAGTCTGTGTCAGAAGAAACAGGACTTGATCAAGCTCCAGCCCTCACCCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAAACCAAGAGAAAGAA[AT]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCTTTTATTCCAAGAAATGGGAAGCG[GA]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24	G A AATGGGAAGC	TTTATTCCAAG	TCATTCAAGCC AATGAAAATG	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT/CJAGGG GCAGGTGTGGGCAGGGTGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59	T C GCAGTGAT	GGCTGGACACT	CCACACCTGC CCT	TTTTTTTTTGGTGAGTGTGTTCTTCAATAAAGAGCAGAAAGAAACC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCCAAACATTGATATTTTGTCTTTTCCCGAGGGCAAAAAGA GAGTCTTCCCAGAAACCTC
WI-13578	48	T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACTCAAGAAATTGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTGGTCTCTCTCTT GAGTCTTCCCAGAAACCTC
WI-13789	62	G A AGGGAG	TTGATGGCTG	CAGTGGCTTC CTCTGTTT	GAGTCTTCCCAGAAACCTC
WI-13594	66	G A AGC	TTTTTAACACA GATCACAAA	CCTTGGGCGCA GTACTTTT	AATAACAAGTTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCACAAAAAGC[G/A]TGACACAAAAAGTACTGGCGCAAGGACAAAATAATGCTAAGAAATTAGGCCAACACAGCTGC

WI-15625	40	C T	---	---	GTTCTCCCACTACTCCCGCAGAAAAGGCATATTCAA[C/T]GTGCCATACTAATTTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84	C G A	CCACACTGAA GACTCACCAG	TCCCAACCCCA CCCT	GTCACATTTCTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACCTTAATCAATAATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCT
WI-13600	26	G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCATTAAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89	G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCOCA
WI-13650	76	A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTACATAATTTTCAC TTTTAAAC[A/T]TAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83	C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80	A G AAA	CAATACATTT GCATTTTCTCTA	CATGATACCAC AGTTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTGCATTTTCCTAAAA AAAGAAAGACATTT[A/G]TTTCAGAGAAAACCTGTGGTATCATGTCAGGAAAAGCAGAAAAAATTT
WI-13909c	93	A T	---	---	ACTTAAACTGGCTTATCTTCACGGTAATCTATTTCTGATTTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACCTCGAATATCTTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G A C	TTCCTCACACT CTCTTCAAACCT	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACCT[C/G]AATAATCTTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A	---	---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAACAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78	T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAACAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCAT[C/T]CTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104	G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTGCTTTTGGGAAGACTACCATTTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTIG	TTTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAATCAACTAGCTTGCTTTTGTGTC[G/A]TTTGGAAAGACTACCATTTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTCGGAAAGAAAGTGTGGAAATCACCTCATCTGTGTC TGTAATCTGCTTACAGTCCCTTGGCAAGACAGACATATGTTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTAGTGTTT[C]TTTAAATTATGAACCTTTTGGTGAAATTATGAACGTGACCAAAAC C
WI-15747	88	T C A G T G T T		TAATTT	AAGAAAGCACATACATTTCCAGAATTTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGGGATGAGTTCCTCTCGTTAAGTGCTGGATATACTTGGCTTGAC[C/TT]GGACACCTTTTACG GAGGGATTCCGGACAACT
WI-13752b	117	C T ---		---	AAGAAAGCACATACATTTCCAGAATTTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGGGATGAGTTCCTCTCGTTAAGTGCTGGATATACT[C/TT]GGCTTGACCCGGACACCTTTTACG GAGGGATTCCGGACAACT
WI-13752a	106	T C A G T G T G G A	CCTTCTCGTTA AGTGTGC	CCCTCCGTAA AGTGTGC	AAGAAAGCACATACATTTCCAGAATTTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGGGATGAGTTCCTCTCGTTAAGTGCTGGATATACT[C/TT]GGCTTGACCCGGACACCTTTTACG GAGGGATTCCGGACAACT
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCAACCAATCAACAGTACATGATTACTT[G/CT]GGTTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A A C T G A A	TGGTGCTGAAC GC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCCCTTGCCAGCTAGGAGCTTGTGTATGGTGCTGAACAAACTGAA[C/TT]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68	C T ---		---	CCCTTGACTATATTGTTTTTCCAAATAAGGACTATGTGTAGAGAGAGCCCCCGTACATACCTTAT [C/TT]AACCATTTTCATCCACCATTTGTAAATCTCATCTCTCTGGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A C C A T T C A G C	ACCCTTTCATC CATTACGC	TGATACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACACACTGAATATACTGAATTAACCTTCAACCTTTTCATCCATTCAG C[A/C]AATTTAAACTCTTGCCAAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCACACATACATAGATCAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTGGTTCTCTAAATCGATACATCCAAACTTT[C]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTTATTCAC ATTAAACTTG CACA	GTTCTTTGATA TGTTGGCTTAGT TTT	GGATTTTATTCACATTAACTTGACACA[G/TT]TAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCAATTGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACAGTG
WI-13785d	72	G A ---		---	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13785c	56	A C ---		---	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAGTCGTAGTGACACATAGCTGTCAACACAGTG

WI-13785b	40 C G ---	---	TGTTGTGACAG	TCAAACTGCACACTATAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27 T C TGCTT	CTATGTGTGAC T	AAAACCTGCAC ACTATAAAG	TCAAACTGCACACTATAAAGTGCTTT[C]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88 C G ATAGG	GGCAGGAGGA TTTGTACT	GGATTTTACAT TCAGCCTAGAT	AGAAACCAAGTATATCATAGGCAAAATAAATAGTTTTTACCCCATTTGATACAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCCTGCCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTTCTC	AGAAATGGGCTC TTAACCTTGTA	TTCTCACCCCT TTTCTTTCTC	TAGTCTCCTACAAATTCCTTCAATCCATTTTCTTCTCACCCCTTTTCTTTCTC[C/G]TACAAGGTTAAGA GCCCATCTTCAACAAACAAACAAACAAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTGAACCAT GTGTAGACTGC	CTTGAACCAT GTGTAGACTGC	TCATTTAAGTGCACITTTGAACCATGTGTAGACTGC[C/G]GGCACTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGTAAAGTCCCTGTTTGAGCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACCCTATTCTT	TGAGGTTTTTC ACCCTATTCTT	GTCCTTTGACAAAGTCTCCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTTACCCCTATTCTTC[C/G]A JTAGACCCCTGGGAGAAACACACATGTGTAAAGTGGCTCAGGCACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	CAAGCTGAATC TGGGATCTC	TCTTATAAAA GGTCAGAGGC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C]GAGATCCCAGATTCAGCTTGCTCATATAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTATCCTGAACATTCITGAAGCACGAA
WI-13446	22 G C TCACTCATCA	AAGGGAATCA AAATCAGAAG G	GCCATGTTCTT TCACTCATCA	TGCCATGTTCTTCACTCATCA[C/G]CCTTCTGATTTTGATCCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATTTCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56 A C TGGGTGOC	CCTGCTGTCTC GGOC	TGAGCACATA TGGGTGOC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGTGCC[C/G]GCCCCGAG ACAGCAGGATAAGTTTCACAAAACCTTGACCAGGCAGGTAGAAAGCAAGGCATGGTTCAGGATG
WI-15702d	107 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAA[C/T]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAA[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAA[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C	AACAAAATAA AGGCTTTCAA	CCTCACCCCTT TACCCC	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAATGGGTCTTTTGAACAAATAGTTTT TGA
WI-13831b	113 T C	---	---	TTTTTTTTATGGATGCACCTGTACATGTTTTATTAGCGAAGGTGACTTGGAAAAGGAGATTACACAT ACTTCCACTGTATCCTCCGGGTAAAGTTTTCTCTCTCTGTAGAT[G/C]GTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13831a	56 G C	---	---	TTTTTTTTATGGATGCACCTGTACATGTTTTATTAGCGAAGGTGACTTGGAAAAG[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGGTAAAGTTTTCTCTCTCTGTAGATGTCCTCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13806	62 G A	---	---	TGATTGAGCTTAGAAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAACTAGGCCTCAGGT[G/A]C CCATTAAAGCATGCTGTGAATGCAAAAGGAAAGCTTAAAAAAATTTTTTAAAGGTGACTCCAGTAAA CAT
WI-14372	86 A G	---	---	CACATTTTCAGCAACAAATCGAGGTGCAACAGGGTTTATTTCACATTAATATTAACCTGGATTT TTTGTCAAATAAATAGGGA[G/G]TTCTCTTTAAATAACCATCTCCTCACTTCAITGGCCAGT
WI-14373	95 A G	---	---	AGGCTGTTTTTTGAGGCCTGAGGACCCCAACATGACAACGTAAAGACTGTAAACCATGGTCATGTGAGTT ATGAGCTAGGAACCCCTGGACGAAACCA[G/G]CACATATACAATCATCTCCACCTCCCAACGCCCTTT ACTTTCACAGCCTCTGCA
WI-14078	61 C T	AAAGAAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCAACATGGTGTATCAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47 C T	AGACTTGAGA GCTTAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAACACT[C/T]ATTTGTTATTTCACAG CTCAGTAGTTTAGAGGTCCAGTAGGCTTGGCTGAGTTGTTGCTTAAGGTCCTTACAAGGCCAA
WI-14085	31 A G	CATTTATTTTC ATGTGTAAGA AGAAAA	CAGTCATGTTG ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAAGAAACAAAC[G/G]TAACTAGCACGTGAACATGACTGCATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAAGTGAGTGAAACAAATAAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCCTT
WI-12169	121 G C	AATAAAACTT CCTATTTTCTT TTGCTT	GGGTCTGAGG TGAAAGAAAA A	GTCAAAGGTGGCAAAATTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTCATTCTTCTAAA TTTTCACTTTTATTGCTAAGTTATAAAATAAAACTTCCTATTTCTTTTGCTT[G/C]TTTTTTTCTTTCA CCTCAGAACCCCTTA
WI-15705	50 A G	GGAGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGGAGAAATGAAGGAGGGAGATTTTAGACTGAATC[G/G]TTCTAGAGTATTT GACGACTACAGCTCCTCTCTTTGTACTACGGAGACCCTGCTTATAGCCCCCAACAGGAAATCCTCA TCTGCGGTTGCCAGACAG

WI-14379	102	C	T	TCTATTAAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTGGTTGTTTCTACTGTGGTGGTCTCGCTCACTAATATCCAATCCTAGTATGATTTTCTTT TACTTGTGCTATTAACAGGGTTATGTCACACC[C/T]TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAGCAGAAA[A/C]A]CCACCATTAACAAGAGGACACTGCAGAGGCTTATGTATACA ACACGTGTCGCCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C	A	---	---	ACCGCAGAGCTGCTGTATTTAAAA[A/G]ACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACCTGCTCTGCTCTCCAGGACTCTTCCCACCACCCC
WI-15937	24	A	G	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	TGAACTGAAACGTAATTCCTCCA[A/C]ACACCCGTAGAAACTTAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGCAAAAAGGAAGTTTCAGGTGATACAAGATGTCTGCCATCACACCTGAAAGGAT GGTT
WI-15944	24	A	C	AAACTGAAAC GTATTTCCCTCC	GGCCTTTAAGT TTCTACGGTG	ATGTTTTATGATCAATTCCAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAGCTCAGTCACTAC
WI-14124	92	A	G	---	---	GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTTTGACGACTA[C/T]GTGGCCATGCCATTCTGTAAAGTGAATTAATGAACA
WI-14125	88	C	T	GGTTGACCTG CATAGATTTT	GGAATGGCATG GCCAC	GTTTATTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14136	120	G	A	GCCTTCTCACC ATGCTCTCACA	CTTGTTCTGTC TCCTTGGGC	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTGGTTTCAATG
WI-14138	23	C	T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTTCAAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTATATTCA GACAAATC[G/A]AATATTACTTAGCCTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74	G	A	GACAATC	TAATATT	TTTTTTAAGAGTGCCTTCACATCATTTATATTGATTGACACAAACTTTTTTAACCTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953b	59	C	T	---	---	TTTTTAAGAGTGCCTTCACATCAT[T/G]TATATTGATTGACACAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T	G	TTTAAAGAGTG TCCTTCACATC GAT	TCATCTGTTCT TGTTGTTTTTG A	TTTTTTAAGAGTGCCTTCACATCAT[T/G]TATATTGATTGACACAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

WI-14631	82	G A ---				TGAATTCATGGACAGTTTTGCCCTCTGTTTTAGTGAAACCCCTCACAAGCACTCTGCATAGTCCGCTTTCTGCTCTCTTTAAC[G/A]TGCCTGGTCCCTCTGCCCAAACCTTTTAGGATTGGCCCTCCTCAGGGCCTTGTCCTGA
WI-6053	24	A G ---				ATCACACCGTGTCTAAGAACAAAC[A/G]TCTTCATGTCCAACATCATATCCCCGGGACCTTTGTCAACTGCAGTACACTTCCCTGCATTGAACCTGGCTTCCCTGGAGGGAAGCCTCTAGAGGCCAGGTAAGGGGTGCAGCAGTGAGGGGTATATCTGGCTGGCCAGTTGGAACCCACGGAG
WI-15964	99	T A CTGGAGGTA	GCTCTCTGTCC	GACTTCTCCAC	CCTCTTGC	CAGAAACCTCTTCTGTGTATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAGGCAGGAGGCTGCCTTGGGAGTAGTAAGCTCTCTGTCCCTGGAGGT[A/T]GCAAGAGGGTGGAGAACTCTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG	CCCCTTCTTTC	TCTTCCCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAACAAAGCCAGGCAATATACCCCATCAGAGACAGTGACAAGAGCAGCTGGGGCACGGGGGAGGC[G/A]GAAAGGAAGAGAAAGGGGAGGAGCCT
WI-12179	96	G A TGGAGGTCA	GGAGGTACGG	TCGAATGACCC	TGTAGATGC	TAATTTAAACACGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCCTAGAAGGACATGATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	CAAGAATCAT	GGAGATATTGA	CTTATTT	CACAAATAGTGAAATTATCTGAGCAAGAAATCATTTCTCATTTAAATTTGT[C/G]AAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAAACCACTGTTA
WI-14666	105	T A ---				AATGTGGACTTTCAACAAAGGGTTTAAACTAATCTAATAACAACCTCTACAACACATTTCCAGAGCATATAACAAGAAATTATTTACAGGCAGCTAATGTATTAA[A/T]AACCATGAAAAGAAAACCTTG
WI-13473	31	C T ---				ATCTAGATGTCAGCAATGGGCTGAGACTGT[C/T]TGTCTGGTAGATGCAGTGTGTGTATGTTTCTAC
WI-13967	103	A C AAATAAAAA	AAAAGACTAC	TTGTGTTTCA	TG	TCTATTACAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATACAGTCAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCAATTCAGCAGTCAATTA
WI-14408	60	T A G	GCAGACACAC	TTAATTGTGTA	TTACTTT	AAAAATAAAAGACTACAGATACAAAGGAAATAAAAA[A/C]CACITTTAGGAGATGAAAACACACAA
WI-13683	47	C G ---	TATTACAGGCT	AAACTCATTG		TTAATAATTCAGCAAGTTATTGCAACAGGTTGAAATGCAGACACACTATTACAGGCTGT[A/J]AAAGTAAATGAGTTTTACACAATTAAATATTAAACACATACTTATGGGATTTGTTGAATGA
WI-13910b	63	C T CGTCT	CACCATGGCA	AGCACACTTAT	CAC	TTTTGTGTTAAGAACAGCATTTTGAAAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCCTTTTAAATTTGTAATATTATATAGTCGTTTTATGGTACATATTGATTGTC
WI-14635	22	G A ---				TTAGAAAACGTATAAAGCAACACAACTTTTGGGAAAGCACCATGGCACGTCTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
						ACATGGCAGATACAGAGCTGT[C/G/A]TCTTGAAGACCACCACCTGACCAGGAAATGCCACTTTTACAA
						AATCATCCCCCTTTTCATGATTGGAAACAGTTTTTCTGACCGTCTGGGAGCGTTGAAGGGTGACCAGC
						ACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCACTTATGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A G A	CCCACTTGAAC TCAAGTCATC A	AAACTAAAC CTTTGTGCCTA AAA	GTGGAATTTTATTAAGCCATCAAAATTTCCCTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCA[AG]TTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73	T C	GC GTTTGACTT GTGGGG	TCCACACTGC OCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATTTGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCGAGTGTGGACGGGAGGATTGCAACCAGAGTTTCATACTG CAA
WI-12535	50	A T TAT	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAAGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[AT]CTTCCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTGTTATCAGCTGAGAAAGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G A GGGAA	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCAATTATGCTTGGCTTACCAATTTTTATAGCTATTGGGAGGCAGGAAAGGAAATTTGGC CCAGAAACCATGAGATTTGGTCAAGAAAGGCACACGCGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C ---		---	ACACAATATAATTCCAT[T/C]CGAGTGATTAAACCTATTTGTTGTTTAGAACCAAAACAACACTAC AAGAAACATTTTCAAACCTTTTTTTTCAGGCTGA
WI-14808	52	T A CTACCCTGT	ACCCACACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAGTACCCACCACACTACCTGT[T/A]AAAACTCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAACACACAACACTGAAGGCCCATGTA
WI-14816	29	A T ---		---	AGTTAAAAAAATCGAGTCAGCATTTATTT[AT]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T TTTAAA	GCTATTAGGC AAACTGAACA TTTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGT[C/T]ATCCATGTGAGGGCTCTAG ATCATGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T CAAAAA	GGATACAGCA GTAAAGAAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAATA

WI-14836	28 T C ---			TC TTGAGGGATAGAGACAGAGTGTTCGTTGATTTTCGGTTTCAGTTGGTTGTCATT GGTTTGTGTTTTGCTAATTTGCCCCACCCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60 A T AA		TGGTGACAG GAAATACTT	ACATTTCCCTTATGATAGCAACAATAATATGATGGATGGTGACACGGGAAAATACTTAATTAATTA AGTTGTAAAAGTAGCAAAATAATGAGTATATACTATAAGTGATAGAGGATGATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---			ATGGCAATTTACTTTATAGCAATGAACAATAATTTGTCAAAGGGCAATAATTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTACCACAAAGCTAGAGGTCAACAGTACCCTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A		GACATTCCAA GGCTCTCTAAC	TTTTAATTAACGTA AAAAGGCAGGACATTC CAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14733	98 G A A		CCAAATTGAC AGATAATTCTGC	ACGGAGTCGTCCTGATGATTTCTGTCAAAAAATGTTGCTGATTTCTAATCATGAAGAACAATT AGAAAAATCCAAATTGACAGATAATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGA AAAACACAAAA
WI-14898b	79 A C ---			TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[A/C]JAGGTGCCACTAAGG ACTTCTCCAT[A/C]AAGCTGCCCTGCTGTGCACGTTGCCCTGGCTTTGCTAACCCCTGGTGTGCATCT GCCGTGTTCTGCTT
WI-14898a	50 A C CA		CATGTACAGG AAGAGTTGTCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[A/C]JAGGTGCCACTAAGG AAAACTTCTCCATAAAGCTGCCCTGCTGTGCACGTTGCCCTGGCTTTGCTAACCCCTGGTGTGCATC TGCCGTGTTCTGICTT
WI-14907	48 G A G GACTCTGAC		GGCACACATT GGACTCTGAC	TGGTATTTATTTCCGACATTACTGTAGAGGCACACACATTGGACTCTGAC[G/A]JATTCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTCGGCACACCCATCAATCAGTACTCTGCACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C		CCAATACATT CAGTTCCTGGT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCCCTGGTC[G/A]JAGGTCCCTTTTC CTGGTTGCAGACAGATACCTTGTCTGTATCCTCACATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A ---			CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAATTTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAAACCT
WI-14914	66 G C A		CTGGACACAG TTTTCTCTAGC	ATTTCCCTTATTGGCTGTGTAAGCCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/ C]GAATTTATTGTCCTGGGCTTGATGGCTTTCACAGC
WI-14926	49 T C ---			GTTTATTTCAAAATGACACATCCAGATTGAAATGGGCACCTAGCGAA[T/C]JACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTCAAAATAAAAATTTTCCTTAATCAGGTCCA

WI-16083	89	C T	ATGTTTAAACA CAAACATATC AAGGAT	TGGAAGAAGATT OCAGCC	GCATCTTTATTACACAGAACTCATTTATGTCCTTAATCATTTGTTTAAATATAATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55	C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGGTATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47	T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACA[T/C]CTCTAAATCATCCCTCTA GATCAGGGAGTCAATAAGGACCATTAAAGGCTCATTACACACAGTACTTTTATGGAAGGATT
WI-15987b	80	A G	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C T	CACAATTAAA GGGTCCAA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGTCCCAA[C/T]GAGGTTGGTAGTGCCCTCCACTATGTGAGGA CACTAAGAAGATGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T C	AGGGAACCTG CTAAGTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTTCTTATTGCCGTTCCCTTCAGGGAACAGGAAACTGCTAACTTGTGAG[T/C]TCCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTAAAGGCTTGTCTCCCTCCAGCTGA
WI-16100	52	A G	CAAAAAGCTA TTTTCCTACAC TTGA	ACAGGAATGTC AGAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83	A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTGAT TTGGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATTCAACTCTAAAATTCGAAGATGAAAAATAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAAACCCAAATGAATGCAATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAATTCAAGGA
WI-14976	35	C T	GTTGATTTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAAATTGGTTGATTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGCATAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATT[T/G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTAAATCATGCTACCAGCCCATCTAAGCCAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCAACTGATCGGAAAGAAACGTA
WI-15002	72	T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAATGCCCTTCTTGA TTTCC[T/A]TTCAGTTTAGGCCTCAAATGGGCTCTCCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90	G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAAGGTATAGAAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT	CACTGGACATA TTCCTACCTG	ATTTGTTGATTTGGTTAAATCTTATCTCTTTTTTATACACAATACTTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCCAGTGCACAGAGGACTCACACCTGTGCATAGACAGCACCC
WI-14683	91	A T	AAGGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAAATTGCAAGT TGGAGTTCGTAAGAACTAC
WI-13470	100	C A T	CCTGCCTTTAT ATTGGAATTTT	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTTATATTGGAATTTCTA[C/A]JAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA[T/A]CTCACAATACCATATACAACATACT TTCAATCACAACTCAAATATAAAATAACCTACAAATCACATTGC
WI-13712	40	A C	TTTACTTTGTT GTCATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTGTTGTCATTTTATTCTATTG[A/C]ATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTAAGTTAATGTAAATTGGCAGCATT GCCCAAAGTTTAAAGAGGACTATTCTTTAAACAAAGACAGTGTCTGACATTTAATTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGTCATTTGAGTGTCTTTATTATATTGGGAATTGCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTTGCTCTCTCT[T/A]JTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C GATTTT	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C]CATCTT ATTCACCAGGACACACCCACACGCACAGTAGAACAGTTCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---		---	GCAGAACCAATTAA[A/G/A]AATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---		---	TGTAGTCTTCAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTTCCAGTATCATGTAC GCACTAAAAAAA[T/C]GTGTGCTTGCTGCTGTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C	TGAAGATTAA CCCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCACAAGTATACAGATACTCTATAAAACCAACCCCTTCAATA TTACACTAATGAAGATTAAACCAGAGTCCG[A/C]TCTCTTCAAAATGCACACAAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATAACAGCTTTTTTTCATTGAAGCTTT[G/T]TACCT TACTATACTCTAGGCTATTTGGAGTGTCCCCAC

WI-15100	74	G A ---				TCATTACAGCCAAAGAAATACCCAAATTATTTCCAAATAAAGCAAATAATTGGAACAGACTGGA GTGAGAAAC[G/A]GGTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT	CCTTTATTTTC CCAAATATAA	GTCACCATGTT ATATTTTCTTT TAAGAC		TGGTACAGAATGTTTAAATTACAGCAGGGCAGTGATTCAGTTAAATAAAATTAAAAACCTTTATTTT CCCAATATAAAATTACTAAATTAA[A/T]GTCCTTAAAGAAATAATAACATGGTGACAGCTTT
WI-12002c	89	T C ---		---		TCCTTAATTTTATCGGAATCCAGGACACACAAGAAACACCCCAAAACCACATGGAGACAGAAG ACGAGACACAACCTCCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---		---		TCCTTAATTTTATCGGAATCCAGGACACACAAGAAACACCCCAAAACCACATGGAGACAGAAG AC[G/A]AGACACAACCTCCTCCCCACTGCCCTCCTCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA	TCGGAATCCA GGACACAA	TGGTTTTGGG TGTTTTTCTT		TCCTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAACACCCCAAAACCACATGGAGACAG AAGACGAGACACAACCTCCTCCCCACTGCCCTCCTCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-15116	96	C T GTTGCAGTAA	GGGAGCCCTA GTTGCAGTAA	CCTGAATATGC AATTATTTATT ATGACA		TTTTCAATTTATTTCCAGAAAGAAATCACAATTTTCAGTAACAACCTTACATATAGAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCTATAATAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37	C T AATGGGAA	GGCCTAAAGG AATGGGAA	TCAAGCGACCA CCAACAC		GCAAAAGCAAAGCTATGGAGGCCCTAAAGGAATGGGAA[C/T]GTGTGGTGGTGGCTTGATACTTGGT GCTTGTGTGCATGGAGCAGAAGTCTTCTGTCATGCAGGGGCGTCACATATTTTAACTGCACATAAT TTGGCAAACTGTCATTC
WI-15153	40	A G GCATTGCA	CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGTCT T		ATTTACAGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCCCTAA
WI-15215	84	G C TCAAATGGG	TGGCTTTAGAA TCAAATGGG	CCAACAGGGGA AAAAGTCA		CCTTTGCTCTCTGAACCTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTCCCTGTGGTGGAAAACTCTGTGAGGGTTTGCA
WI-15225	80	C T C	CTTGAGGACCT AGAAAGCAAA	TTTGATTGGCA TAATCACTCC		AGGAAAGAGTGGTAAAGCAAAGGCGATCATTTGGATGGAATGATTATGTGTACGAGCACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAAATTGCAAGTTGGAGATATGCTAAAA
WI-15152	51	G A ---		---		AATTTGCTAGTGCAAATGGACCCAGAAATTGGAAGGCTATGTAACACACA[G/A]TATGCACACCCAC AGCCATGTCAAGTGCACAGATCCTCTTGTGCATTCAGCTTTCTTAAACACATCAAAGGCTGCA
WI-15123	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAAACAGAC		TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACACAGATAAAACACAAT

WI-15182	49	C A	GCACAAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAAACCAGGGCAAAATA[C/A]TGTCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTTGGC ACTATG	ACTTATCCGTC AGCAGAGTAG	GTTGACCTCTACAAGTACCATGGGCCCTTGGCACATATG[C]CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT TGAT	GTTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAATAGCCATTATTGAGTATTCTTGTCTTGTAT[C]GTCTACGTAAAGCATGTAAGACT ACAACTTACGACCCATCTCTTCAAGAGGAAGTCTGTATTATGGAAACAAATTTTGTTCATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATATGCCCTACATATTTAGTGAAGTACACCCAGATATTTTTGGGAGAAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAT[A/T]TGGCAGTTTAACCATTTTCAAGAGT
WI-15239	57	T C	CATTTGCAAT AAACACCCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAGATTGTGCATTTGCAATAAACACCATCAT[C]CCTGAG TCCACAGATAAGTCCCGGAGAGGGCTTCCCTCTCTCTCGCTGGTGGTGGCTTCCAGCGT
WI-12634	52	T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACGTGTCTAGCAGTATTA[C]GTCTATTAGCTA TGTTTACAAATTTGTCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTGTATTCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA AA	GAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTT[C]TTGTTAAATCTCTGGCTTTCTGGCTGG TGAGGAGCACAGGCTGGGTCTTCAGGTATCCACTGGTCCCGCATCTGTCCCTCCACTCCCGAG CCACATCTTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAATGC	CCCTCTCCTCA GTGCACITT	CTGTCCGGGGAAGACACCGTGCAAATGC[C/T]AAAGTGCACGTGAGGAGAGGGAGGGTGTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAA AGTGGACATCC T	TCCCAGATTGTATGAAATGCCAGTGGCATTAAGGATGC[A/G]GTAGGATGCCACTTTTAGTAGC AACCGATGTTAATCACTACTCTCATGTTAGGTGCTTTACTTGGATTATCTCATTAAAAACCCACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAACCATGCTGTAAACAGCTGTGC[G/ T]CCATTAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGAGAAATTTAGCATAAATCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG GA	TCCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAATGAGCTGGAGAAATTA TCTG
WI-15325	39	T C	CATGTGGCTGG GAGC	CCCTCCACCAT GATTGTGA	AAGGTTTAAATGGACTCACAGTTCATGTGGCTGGGAGGC[T/C]TCACAATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC
WI-13936	123	C T	AGTTGGCATT AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTCACTCCATGGCGCTTCTCACTCCCTATACATTTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATC[C/T]AACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T	G	TTTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/TAAGAACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C	A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/ACCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G	A	---	---	TTTATTGGCTGTCTGTATAACAATGTGGTGAAAAAC[G/A]TCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTGAGGCACATAGGCTGATTATCAGTGG
WI-14580	100	G	A	CATCCCATCT GTCTTGCA	CCGACCAAGAT CCTCC	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACCTTCAGAACTTCTCAAATAC CTAGTTATTATACACATTTCCCATCTGTCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAAACA
WI-8540	73	T	C	GGCTGCAAT GGCTTA	GGCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTA[T/C]GTGCCCTGAAAAAGAGGCGGACCTCTTGATAAAGAAATGTCT
WI-8039b	97	T	C	---	---	AAGTAGAACACAAATAGAAATGGCTCAAAAATATCAGAAATGCACATCGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGTA[T/C]GTGCCGTGCATGTCATGATTAATAATCCTTCT TACCACAGTCACTTAAGAACCAAGCTTAGGACTAGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCACACCCACA
WI-8039a	87	T	C	---	---	AAGTAGAACACAAATAGAAATGGCTCAAAAATATCAGAAATGCACATCGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGTA[T/C]GTGCCGTGCATGTCATGATTAATAATCCTTCT TACCACAGTCACTTAAGAACCAAGCTTAGGACTAGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCACACCCACA
WI-8044	107	C	A	---	---	CACAACTTCAGAAATTTTCTGCATTTGTGCTTCTCTGATGTCTAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCATAAGGTTTCTCC[C/A]AGTATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTTCTCCAGTGTGGAC TCTCTGTTGTCACAAGAATGGAATTCGGCTGAATGCTTCCACACT
WI-8550	32	G	A	GGGAACATCA ATGCAACAAG	AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AAATTTGTAAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCCTCAGTGAA
WI-8057	87	T	A	---	---	TATTAGATAAAACCTTTTGTCCCGATTTCAGGATGTTTAAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAG[T/A]GATGGACAGCAGCAGAGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCTCACAACTGCCCCCTGTTCAGAGGGATGCTGCCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG

WI-6375	28 A G A A	GGTTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAGGCGAGTGAGACATCAACAA TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTTAA[T/A]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTTAAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTCAATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCTGTGTCGG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTCTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATAAAAATTACATGGGCCTATTATTAAGGACATTGTGTAAATGTTTCCACTTTGTTTTAA [C/T]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTTACATGGGCCTATTATTAAGGACATT[G/C]GTAAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAAGACATACTGCCAATAAAGTTTAAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAAGATTAATGGAAGAT ATCGTGAGCCCAAAAC
WI-6629	75 T C GTCATA	TCTTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTTGTCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T/CJACCCAAACTTGAAGGTGATTGAACCCCAAAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCATTTAAGGAGAGTACTAGGAAAAAAGTACCAACACAGCATGTGAAACAGT TGCGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTATAGCTGGTCTGTGTATACCAGAAAGAGCGGTAICTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACCACC ATTATTAAGG AGAG	GCTGTTTGG TAGTTTTCT	TGCTAAACACCACCATTAATTAAGGAGAGT/CJACTAGGAAAACTACCAAAACACAGCATGTGAAC AGTTGGGCACGGTGTAAAGGCACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATAACCCAGAGAGCGGTATCTGG
WI-6770	53 A G	CAAAACCCCA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA/VGJAATTTATTCAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCAATCTTCCA AAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAAATCAGCTAGCACTAATCTTGACCAAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTCACATTTAAACACATGGTAACTCCAAGCATTCT TCCAAACAAAGAAT/VGJAACATTGGAATAGTCACTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/CJACTTCTTCTCCAGCTTTTGTGAACAAAC AATTCCTCTAAGGCATCAGAAAGCAGCTGAGTGCAAAATGGTTGTTTCAGGTACAAGGTCTC
WI-6844	225 T C		---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGCCATCATTAAAAACAAAGGATTTTCTCCTCTTG GTATTTTCAATGATGATTATACAATAACGAAGTTAGAACTTAAATGCACCCTGATTAAATTATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTTCCTTCTTCAATAAATGGAAATTTTAA TATTTCTGTAGTCTTGAGGT/CJATCATTATGAGTAGTGCAAGGTG
WI-6824	112 A G		---	CGGTTTTGTACACTTAATGGGTTTTTTTTAAGGGATTTTTTTCAGGTCTTGTCAACAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCGCAA/VGJACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGCTCCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAAGTGGCAAGTAAGGCAATTTCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATTC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAGAGGCCAACATGGAAGTGTCAAGAAAAACATTTCTGATAGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/CJAGAATAATTAAAGCCACAAAGTGAACCTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C		---	TCCCCAGCTCATATTTATTGGGCACAGAGTGGGCACTCAATATCTGATGAACCTGATGAACCTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCCGAAGAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTGCCTTCCCAAGGAATGTGTTTCTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCCTT/CJCATGACATTGGACAATAGTACTACTCTTTTCTAC
WI-9413	112 G C		---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACCAGAGCCCTGTCTATATGAAGACAAAC AGTGGCCATCTTGGGTGGAGGATACCGCTGTATTCAGAT/CJAGATTTGGTGGAGGAG ACCATGACAGATGACAAACGGACAGTTTCTCAAAACAGAGGTATGA
WI-9557	74 C T		---	AAAGCTTTAAAAAAAAGTGGTGTATCTTTAGAAACACTTTTCAGCAAGATCAAGTAGCCAGCT ACAGCCT/CJGGTGCATCTTAACCCCTCTCCTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTTCACGTTTCACAACACACGCGTG[G/T]TGGCACAGTCTACCAAGTGCCCGCAGCGCCACGCTTGGCCGGAAGGTCTCATTTCTGTCCTCTATGGACTGATTGAATTTGGGATGGCCAGCTCCAGAATGTTCCACGTGGGGCAGCTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCAAGAGGTTGCACGATGCAGCTTGCAGTGGTCCAAGCCGGTGTGCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAAAACATCAACATTGAGTTGACATTTTGGTGAAGTATAGCTACCATCCACTATCATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAG[T/G]ATAATTCCTTGTAATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAAATTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	CCTCCCAAGTA GCTGGGA	AAAAATTAAAC CAGGTGTGGTG T	CAGGTCCTTGCTCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGCCTCAACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACACCACACCTGGTTAAATTTTTAAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAAACAAACCAACTAAGCAGGTCCTTGCTCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACT[C/G]ACAGTAGCCTCAACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTAACCTCTCTCTCTCTCTCTCTCACTATGTTGCCCGTCTCAAAAAAACAAACCAACTAA
WI-13119a	51	C G	---	---	C ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTTTTTC/TCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGTTTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAAATTGAGGGAATAGGCCAATTT
WI-13112	71	C T	TCATAAAGAC TACAGACTTA AGCTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGTGACACTTTGATAAAAAGGAATTTTAGCTTAGTAGAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACATCTTTATGGAAACTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGTAAA
WI-12988	36	C A	CTCAGTACAA	GTTT	TGCTATTTCATGACAGACACGTGAGACAAAATATTTCTTATTTTACAGATGGAAATAGACCCAGACATTATTCAGTACTTTAAACCACCTAATAGTGGAAACCCTGAGACTTTA[G/A]ATCTGCAAGGGGTTTAATAATGCAATATCACATATATTTCCATTTTAAACACCATAATTAAGTTTCCATTTTCTTAATAGAAAAATGATAAAAAATGTTTCCCAATAT
WI-13020a	108	G A	CTTT	CCCTTGCAGA	TGTATAAAAAATCCAACTTGTTCACAAAGTACATATGTCCTATGATTTTATGCATACATCCATATACATATCAAGGTAAAGTCCA[G/T]ACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAAGTAAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAGCAAGCAAGTGTGTC
WI-12837	87	A G	CCATATACAT ATATCAAGGT AAAGTCCA	GCCATAGGAA ATGCTGTTTTT	AGTGTGTC

L42611b	50	G C ---			GTCCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCCTGTC[G/C]JCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATAATGTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34	T C ---			GTCCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTT[C/C]CTCAGGTTGCCCTGTCGCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATAATGTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAATAATCAATTTAAATAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATAACCATTTTCTGCTTTC AAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAATAATCAATTTAAATAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATAACCATTTTCTGCT TTCATAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCACCTTAATCTGCAATTTTGAAACTAGATTGAAT TCCTTTGCAAAACCCTTGATCATGATGATACCCGAGTTAAACCGTTAATTAAGAGACATTAAACATGG CCTGGTG
WI-1231b	141	G A ---			TCCATGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATT CAACTAAGCAGGAGTGTTCACAATAAACAAACATAGGCTCTTTATTTCTCCTTCTTTCAATTTTCTT TCAC[G/A]TTATTCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTTAC ACATTCGGACC
WI-1231a	126	T C A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATT CAACTAAGCAGGAGTGTTCACAATAAACAAACATAGGCTCTTTATTTCTCCTTCTTTCAIT[C]TAATTTT CTTTCAGGTTATTCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTTACA CATTCGGACC
WI-472	114	G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTCTTT TCCAGCCC	GAAGCAGGACTGTGTTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACACAGAAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG TTACTCTATTT TGTTCT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTC[CT]AGCCACCTGTGGCATTTCCAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGCATAGCACTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAATAAAAACCAACACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAAC[CT]CJATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGACTGTCTGTGGTATAATGACCCCTGTGTCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGGTAGTGAGCGGAACAGAGAGGTTTTCATTGACTCCTAAACTGAGTAC[CT]A]CAAAACGAGCAGGTGCTCACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGGTAGTGAG[CT]GAACAGAAAGAGGTTTCACTGACTCCTAACTGAGTACTCAAAACGAGCAGGTGCTCACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACCCCTCGGCTTCTCTCACCAGTCCACATGGGTGCCAAACAATCCACATTCCCTACATCCTCCCACTGGGCTGCCTCTTCAACACCTCACCA[A/G]ACTTGGCTTACCGGGAAGCATAAAGCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCC[G/A]GCTGTCTATGTGGGATTAGAATAAATAAACACAAAATGAAAACACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAGATAATACTTCAA
WI-991	37 A T	---	---	TGCATTCAATTATGCACCAAAATAATAACTTCTGTACAT[A/T]CATTATTGTATTTCATTATCACAAAATATAGTGAGGAGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAGTATCTTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTGGAATCCATCAACTGAATCCAGAGAAAAATGTTCTGCATCACTGTACAAACACTGACTCCTTTTCTCCTTTTGAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGACGTGGATACCTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTGTCTCCAG[C]AGAAGTCAATTTGTAGGTGTTCTGCGGCTTTTGTCTAGCTTTCCATTTTCTCTAATACACTGCCTCTTAAGGAGGGCTTGACAGCATTTATCAGATGGCTGTTTGTCTGCAATTTCTGCACTGAAG
WI-5381	178 A T	---	---	TTCATGCAGAAAGGTCCATGAGTTTACAGAATCTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAAATGAGAGTGGCTTGTCTCATGAAAAATTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGAATAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT[A/T]TTACTAAAACACACAAATGTTTAACTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTCTGTGATG
WI-5791b	76 G A	---	---	CTATGTATTCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAACAAGATGAGAACAGGTCCTAGAACCTCAG[G/A]ATCGAAAGGAAGTTTATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTAATAAATAAATAAAGTAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGGCACCCCTGTTTGTAGGAA

WI-5791a	44 C G ---			CTATGTATCCATCTAGCAAAAGCAAGACTATTGGATAAGTTT[C/G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGAAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAGAAGTACATCAGATTGTGCATTTCTTATTTTGCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/T]TATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAG TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5406a	42 A G ---		---	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATTTCTCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCTTCTCCCTCCCTCTCCCTTTATTTCTCCCTTGTCTTTCTTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATAIGGGTAICA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAAATTTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[A/J]TAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAATAATCCAAGAG[C/T]CTTAAACCATAATTTGTGTTTA GAACTCCTGTGGCCAAACCACCTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGAGTCG	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTTACACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGATGGCATCTGTTTCAAC TCCTGTTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29 G A AATTT	CCAAATTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTTACACATTAGTTGATGAATTT[G/A]AATTTTACAGTATCTAATGATGGCATCTGTTTC AACTCTCTGTTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38 T C ---		---	TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCA[T/C]CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C ---			TATTTTCTCAATTCCTGGAGCACACCATGCTCTTCTATTTCATGCTTCACATTTATTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACGAGCCAAACAGCCTCCTCTTCCCTT CCTGGTGCAATTTACTCTTTACAC
WI-5546	40	C C C A A T A C T T T T T C A G G T G A A A			CCTATAACCCCAATACTTTTTCAGGTGAAAAAAGGGAAAA[C]ACCCCATGTTTGCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATTTCTGATGTGGGAATAT TAGAAATTAAGCGAGAGAGGCA
WI-5552	97	C C T T T T T A G A G T			TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGTATGGGT GGGGCTATCGGCACCCAGCCTTTTAGAGT[C]CTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T ---			TAAGTTGATTTAAACACCTCTGTGCCTCAATTTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTCTGATGATGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]CCCATTTTGAAAAATTAAGCTTTTGAATTTGTTTCCA ATG
WI-5573	58	C T A G G T A A G G A G G T G G G A			TCGGGTATTAGGATGCGTTCAACCTCGATGATGGCGGTTTCATAAGGAGGTGGGA[C]TGACAC ATTACTCTCCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A ---			CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCCTCTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA[C]TGGCTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCC TTTTGCCAATTTCCCTGTATATCAACAGAGAGAGAGGTTGG
WI-5850a	92	C T ---			CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCCTCTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA[C]TGGCTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCC TTTTGCCAATTTCCCTGTATATCAACAGAGAGAGAGGTTGG
WI-5612b	125	A T T T C			TGCCCTGATTGACACATAGTTATCTGACAGTAATCAATCTAACATCACAATAATCTTATTTCTGCCCTG TCACACTAATTTGCAAGCAATTCATTTGATTGACTATTAATGAGCATCGTGTCAATTC[AT]CAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA
WI-5612a	44	T A ---			TGCCCTGATTGACACATAGTTATCTGACAGTAATCAATCTTAACA[AT]A]CACAATAATCTTATTTCTGC CTGTCACACTAATTTGCAAGCATTCATTTGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA
WI-5636	26	A C C C G C A A T A A T T G G G A A			TGAGAGCCAATTTTATCCGCAATAA[A/C]TTCCCAAGTCTCGATGGAGGCATTTTCAGAATCGGG GCAGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---			TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAAATCTTTTTTTCATTTATGCATTCTGACTACTCCTGCTCTATCAAAAATTAAAC[G/G]AAATATTAATATTTTATTTACAGAGGAACTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAGACAGACAACTAAATAATCCAGG
WI-5865b	99 T A ---			TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAAATCTTTTTTTCATTTATGCATTCTGACTACTCCTGCTCTATCAAAAATT[A/A]AACAAATATTAATATTTTATTTACAGAGGAACTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAGACAGACAACTAAATAATCCAGG
WI-5865	165 T A ---			TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAAATCTTTTTTTCATTTATGCATTCTGACTACTCCTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTCAGAAAGCCAGAAAAAATGACCAAGACACAGT[A/J]CCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAGAAGACAGACAACTAAATAATCCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTGG ATATGT	CTCAGACATTCAATTTTCATTAGTTGTTAAATTTTGTGTAATTTTCATAGCATGGATAATATTACAGAA AAAAATTT[G/T]ACATATCAAAATGACTGAAACTTACTAGTAGCAATTTGTTTTGTCAAATTTGCT
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG	GACAGAAAAG AGAGTAAATT	CATGGAGCCGACGTTACGCCCTCAGCTTTTCCATC[A/T]TTTTTTCATAAATTAATCTCTTTTCTGTC ACAATGTTCTGCTTCGTAATTTCAACTCTCATTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTG AGAAAATAAGTAAATG
WI-5760b	61 C G ---		---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAGCCGAGTTTTCGATTACACACA GTTGCTGTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAA CATTGTTGAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760	187 G A ---		---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAGCCGAGTTTTCGATTACACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5944	52 A G GGAATCTTG	TTCTCACCATG	GGGTGGGATCT AACTTGCA	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCCCTCACTATTGAGAAGCTAAAGTGTAAAGACTACTCATTTCTCAGTCTTCTCTGCTG
WI-5967b	148 C T ---		---	GAGTTTAAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCCCACTTCACATTCAGCAGATATT CTTTCATGGGTTAATTTGCCCAAGTCATGAGGAGATGCAATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGCGGTATCTGCTCCAATCACCCATTCACCTTTATTTCTCTATTAT GCTGAATGAAACGGTTATATTACAG

WI-5967	165	C T ---				GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCCCACTTCACATTCAGCAGATATT CTTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATTC/TJTGCTCCAATCACCCATTCCACTTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53	G C ---				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCAIG/CJGTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTTCTCTGGAAGTTCOAAGTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAACTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAATAATTGAAAAATTGAATAATTATTAAAGCACCTTCTTAATTAAGCAT CTACAAGGTACTTA/T/CJCACTGTTCTGGGTTTCAATCCTCTTACCTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAATTTGTCTTTT CTC
WI-6450	45	T G TGTCACA	CCAATGACTT ATTCTATATCT		TTGTTTGAAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAATGACTTATTCTATATCTTGTGACA/T/GJAGAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGATTATTTTACGGTCAATGTAATATGCATGTAAAGACTA TTTTACTGGCCTTCTTTATGCATAAAACAAGGATTGGTCTATTCAACAACATGTGTCAATACAG
WI-6461	88	C T ---				CAGTTGTCAATGTCCCTCTGTGACTAGAAATATAGTCTTTATAGAAATATGTGGTTTGAATAAAGCCACA AATTATTCTATAAAACAACA/C/TJAGGAACGAGGCTCAAAAGTGAACAAACGCGCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-7466c	141	G A TTGTCTCTGG	TTTTCACAGTC		AGTCGCATGCC AATTATAATT	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTCACTAGTGAAGTATATCAATAAAGACATGCAAAACCTTTTCACAGTCTTTGT CCTGG/G/AJAATATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCTTT
WI-7466b	80	T C GTC	GACTTTCTGGG CTATGAAATA		TGTCCTTTATG ATAACTAGTTC ACTGAA	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/T/CJATTCACTGAACTAGTTATCATATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTCTCCTTT
WI-9814	104	C A ---				TGCTTTTTAAAAATAACAATGACCACCCTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCT/C/AJTTCTCCTTCAGAAGAGCACTTTGGCCCT CATAGGCATTCCATAGATAATTGTTGAATGAATGTGCTTTTTCATATTTGATTTCCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55	A G ---				CCTCTAACAAAGAAACTTGACTTCCTCAACTCAAAATACCCCTTCTCTAATAATTT/A/GJAGTAACCA AAATATTCTTCAATAAATAATCTTTTAAATTAGAAGAACACAGTGTAGAGGTAGTACATTCA CCACC

WI-9720a	47 A G ---			CCTCTAACAAAGAACTTGACTTCCTCAACTCAAATACCCCTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAACAGAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---			CACGCTCTAAGGCAGGATGIGGCTTATGAGATACCTTTGCAATTGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGCTGCT[AT]GAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTTGCAAT TAAGAATTGCCAGTCTTTTGTCTGTCATCATCTTGAACATTAAATCCACATG
WI-9748	74 C G ---			CCACTTCAGTAAATCAATTTGTAGCATTATTTCTAAAGATTCTAAATTTTATATGTTTACCCCTTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTTTCTGGAATCTTTTCAGAAT TACAGTTATGATGTCCTTTTATATTTCCCA
WI-9943	91 T C ---			TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTTATATCCATCTTC[C]ATTTTAAATTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAAATTTGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C ---			AGGGGCTTCACAGATCCGTCAGCTCAACACTGCCCTCTT[C]AGTGAGCCTGTGAACCCACCAAGAC GGCTGGTCATCAGTGTCATCTCTCTCTTTCCGGACAACATCTTTTAAAGAAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCAATAATCTTGTGTTTAAATAATTCCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCTATTCTACACAAAGGGATTGCAAA
WI-9897b	84 C T ---			CTCAGAAATTATCAGATCTTCCCAAAATGTCATGATTCCTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCTAGCCTGT[C]TAAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---			CTCAGAAATTATCAGATCTTCCCAAAATGTCATGATTCCTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCTAGCCTGT[AT]CAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[C]TACCTCACCAGAACTGGAAGG CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTCAGACA[C/A]AGCCAAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[C]TACCTCACCAGAACTGGAAGG AGTCGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTCAGACACAGCCAAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146 C T ---			CCTGTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCTCCCATTTTCTTGTGTA TTCCCCAAACCAAGGTTCTACCCAACTGATCAATGCTGACTAGTCAATGGCTGCTCAGGGTAA AGCATTTATGA[C]TJAGACACAAAGACAAAGAGGTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGAATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGTTCTA ACATTCAAATAAGATCTTTTGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAT CTAATTTCCCTAAGCACAGTAATCAAGGCTTCTACCCCA
WI-10020b	122	T A	GGGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTTATTGGCGAGAAAAGAAATCATGACTTTTTTTAAATAATACC AGACTAATGATTAAATAAATAAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTTAGTACCCCT CCTAGA
WI-10020a	39	T C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATTCCTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTTATTGGCGAGAAAAGAAATCATGACTTTTTTAAATAATACC AGACTAATGATTAAATAAATAAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTTAGTACCCCT CCTAGA
WI-10064b	170	C T	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA ATAATTTGCAGAGCATCTCTCTCCTATGCACCAAGATAATTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/T]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C A	GTAGCAGGAT CAGGGAAGG	CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATATAATTTGCAGAGCATCTCTCTCCTATGCACCAAGATAATTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C	TCCTCTGTCCT CAAACCTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCAACTCTTA[T/C]TTAATCCATTCAATACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTTATACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCCTGTTTATAATTGGTATCTTTTGGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAACATTAACACTGGTCAGATGTGTTTAAACTTGTGAAACCTGCAGC
WI-10316	104	T C	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAGCATCTATATTATCCAGTCACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTCTTA[T/C]TAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCCCAGCC
WI-2572	61	C T	---	---	AGTGAGTTGTGCACAAATTTGGAGACATTTCTGTGACCCCAACTTAAACACTTCTCCCCACA[C/T]AC AAAGTTAACACTTCAGTTACCAGGTGAIGATTGAGCAGA

WI-10368	31	C	T	TGAAGCAACC AGGTCCTGTT	CAAGATAATTAT ATTTATTTCTCT AAGAGGGG	GAGGAACCTGCCTGAAGCAACAGGCTCTGTTTC/TCTACCCCTCTTAGAGAAATAATAATATCTT GAGATAGGAGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTCTTCTACCCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTTTCAGGG T
WI-10391	32	A	G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGCTCAGGTATGACTCCCA/A/GTCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGATCTGACACAGCCTTTTGTCTTGCTTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146	A	C	GTTACCCAGA GTCCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCCTGACTTAGCGGGTGCCTCAATAATATTCTTTTTCATATT TTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCAA/A/CJAGCTACTGGAAGCGGCAAGAAATTTAACCCT
WI-10567b	82	A	C	---	---	AGCGATGAAATTTATATGTTATGCCCTGACTTAGCGGGTGCCTCAATAATATTCTTTTTCATATT TTCCAATTATTAAT/A/CJCTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCT
WI-10567a	60	T	C	GGTGCTCAAT AAATATTATT CTTTT	AAATTTCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCCCTGACTTAGCGGGTGCCTCAATAATATTCTTTTTCAT ATTTTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCT
WI-11153b	84	C	G	CAAACTTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTTCTATCTCACCTAAATTAATG[C/A]GTGATTAATAATATACATTTTAACAACTTCAAA TTGCTTTAAGTACTTTA[C/G]GAAGACCTTGACTGTTGGATTTTGGATTTTCTTTTCTTTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33	C	A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTAATG[C/A]GTGATTAATAATATACATTTTAACAACTTC AAATTGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGGATTTTCTTTTCTTTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125	T	C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCCAGT	GTTGTAAACTCCAGTATCATTTCCCTCAAACCACGCTTAAATCACAATCAGCTTTTCTTCTGTA GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAAGAAATTGATCCTA/T/CJACTGGG ACTACAGCCATGGAGAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C	T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAACACACACAAAAAGTTTCAACCAAGTGAATTATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTCAAGTTCAATATTGT ACCTACAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTTCTTTTCTTTTGT/GTCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGTGCTGCAATGGGAATATTGAAACCC
WI-10656	59	T	G	---	---	

WI-11169b	154	T G T T T T T	TTAACCAAGA GTTTTTCATTG	CTAACTTAAAA ATCCTCATTTCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTTAAGCCTAAAGTAGTGTCTTTTAAACCAAGAGTTTTCATTCTTTT TTTAAAAAAGAGCAGACAT/GJTATCATGTGTCTGATAATTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A G T T G A A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTTAAGCCT/A/GJAGTAGTGTCTTTTAAACCAAGAGTTTTCATTCTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTCTGATAATTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G	---	---	CAAGTGCTTGGACCTTGGATAGGTG/A/GJACCGGCTGAAGTTGGACAGTTGTTGGTTAGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCCTTTTGGGTTTACCCTAGGGGTCACATAAG AGAGATGGGAGACAGTCTCAATCTGTCTAAATAATCCAAATAGCCATGGGTTTGGACAAATAC AAGTTAGTGTCTCTAACTTTAATGGGCATA
WI-10686	133	C T A A G G	TGCCCCCTGTCC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAAACAAGATGATATAGTTCTGTCTAGAAATCTGATGCCCCGTGCCAAGG C/TJTGCTCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77	T A A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TCTTTTTTGAA AA	GGTAGGATGATTCTAGAAATGCCACTTTACAGCCACTGAAATATATTGCCCTCCAAATGATTCTTTCTG CTCAAAGAGT/A/JTTTTTTTAAAGTTATCTACTTATTTATTTCTGCTTTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTCAGTATAGCAAAATTAATTAATAAAGTAAGAAAAAGAAAGGCCAATT TGGGC
WI-10694	144	A G T A T G A G T T T T C	TGCAAAATGCTT TATGAGTTTTC	GGCATTITGTA AAGGAGGAAA	TAGAGAGGCTTTTTCAGTTTCAGGGTTGGAGGGGTGGTGAAGTTCAGTTCTCTAGAAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAGAACTCAGTTCTAAAGTGTTCAGTCTTTTGCAAAATGCTTTA TGAGTTTTC/A/GJTTTCCCTCTTACAAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCTGCCAGTGCATGGAGCAGTG
WI-10719	115	T C G C C A T T C T A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCTATTAAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAGT/CJGGCTGCTGGCAGTGCTT TCCAGCCTGCTGCCATAACTAA
WI-10721	40	A G C T T G C C A	TGGCTCTGCTA CTTGCCA	GAAACTCCAC ATAAATAAT CTCA	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCA/A/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTTCCCTGCTTAGGTTTGAAGAAGTTGAA

WI-11204b	88	T C ---			GCACAGAAATTGATTAAATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAGAAAACTTTACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-11204a	80	T A AACTT	GTAAAAAGGG TGAAAAAGAAA	TGATCACTTAA AATGTACATAAA TACCTTT	GCACACGAAATTGATTAAATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGTG AAAGAAAACTTTTAAACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-10732	80	C A ATTGGTTCACT	GCTGTGCTCTTC CTGTATGTACA	AAGAAACAATG CATAACAGAA CTTTAA	ACATGTATTTCCCTTAGTGGTCAGCCCTTCCCTTACCCCAAGAAATATCCCTGGTTTATTGCTGTCTTC ATTGGTTCACTTC/AJTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTTAAACCTGC
WI-11206	127	A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGTCTTTTCTTTGTACGAGTGTATAAAGAAATTACCACTCTGTACACATTTTGTAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCAACATGAGGTTGTGTTTCTGTATGTACAACTC[A/T]CCAA CCATTAGGATTGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATTCACACACATGGA ATAAGTCTA
WI-11215	68	C T ---		---	GAAAAAAAGTTTAAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTTACAGATTTTATTAGT [C/T]ATTTTCTTCTATAATATTTTCTTGTAAAGTGATGGATTTTCTATAAAATTAAGGAAACAGATATTT ACACAGAGAAAGACAGGATTGCTTGAATTAGTATAACATTTTATTTCAAGCCCCCATTCACCATGT TTT
WI-11219b	89	G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTGAGAGAAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18	G A ---		---	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136	G A GGCTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAATGCTAAAAATTGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACTGCGGCTG G[G/A]TCACAACCTTGGCTACCGAGAGAACCTGACACAGACTTCGTAATTGCTTTTACAGGCTACTGG AAAGCC

WI-11222a	25	C T A	GCCACAGTGG AATCATTAC	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGAATCATTTACACTA[C/T]CGAAATCAGCAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTTGTTTTCCATAGACCCACCGTTGAACTATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGGA AAGCC
WI-10775	39	C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAAATTCATTACACTC[C/T]ACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCTCTGGCAGATAATCATTTGTTATCATTAGACATTGCA GGAACCACCATATGGATGGATAAATGTGTTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAAATAATCTTCTTATAGTTGAATTTTAAGTAAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAAGTATAGTAACAATAAGTAATTAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCCACAAAATTAT TTCATGA
WI-11226	165	A C ---	---	---	
WI-10778	62	A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGTACTGACAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTACACAGCAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21	C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TGGACACACTGCTCTAGACC[C/T]TCCCAGGGTCCCTCAAAGGTGGGTGTAGAGCCCTACTGCCCT GCCCTGGGGACGCAGAGGCATCAGGGCCCTTAGTCTCTCTGGGACAGTGAAAGGGCCACCACC
WI-10810	58	C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAAAACCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGCAGGAATT[C/T]CATTT CTGTGTTTCTTAGGGTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACTACCCCTAGAAAGTCATGCAAGAGAAATGATGA
WI-10828	23	T C ---	---	---	GGACCAACAGAAATTAATGGCA[T/C]JAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGCATATCTAA
WI-10832	91	G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAAATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGAGGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCCG
WI-10834	96	C T GTGTTAAT	AGAAATTAAC GTTCAAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTTGCCCAAGACCATTAAACAAGATTTAATAGTTAAAGCCAAAACATA AAGAAATTAACCTGTTCAAAAAGTGTGTTAAT[C/T]CTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T C ---	---	---	GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCTCTTGCAATCCCAATGTGTAAATTATTTATTCT TGATATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCCT

WI-2296	81	A	G	GA	TGTTACTTTGA TTCCTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTAGAATAAGTTGTTACTTTGA TTCCTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTGCAGAGGTTACATTGTTGTTG
WI-2300	77	G	T	CCAGTCATAC	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTTCCCTGGAAATTTCCCTTAATTGAGCGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T]TGCTTTAAATTGACCCCAACCATTAAGAAATAGCATTCA
WI-2371	55	G	T	CCCAGCTTCT	GTCTTGTTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGTCTGGTCTTGTCTTCCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTTCCCTTGCTTGCGAGCTGTATAATCCCAATCCTTGCCCTCCAGCTTTACATGATGT TCTCTCCGIGTGTGTG
WI-2395	122	A	C	TACTATCCAA	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAAAGATAACATAGAAATATAAATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTGTAGAAAAAATACTATCCAA[A/C]CTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATATTATTAGTAACAATCTTTA CATTACACAAACCCCA
WI-2437c	192	G	A	---	---	---	CACCAGCCACCACCCTACAAACCCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGT[G/A]GCTGTG GTGCCAAGGACGCAATTATG
WI-2437b	179	G	A	---	---	---	CACCAGCCACCACCCTACAAACCCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2437a	128	G	A	---	---	---	CACCAGCCACCACCCTACAAACCCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2440	71	G	A	TTTTAGTT	GCAACCTACT GACAAATTTAA	AACAACCTGTC TATTGGTCTCA	CAGTAGGAAACGGGTTCTCCTTAGACCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123	T	C	GAAAAA	TGTTTAGGAA ATAATGACAA	TGGTTACAACCT GTACCAAAACAT	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTAAATACAAACACAAATGTAATGCT ACATAAATAATTGTCATACTATAATTGTTTAGGAAATAATGACAAAGAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
WI-2886	46	C	A	GGGAGAAGA	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG[A/C]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGCTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGAGGGCTAGGCAAGGAAAGGTGTGAGAAACACAGAGGAGCGTT

[illegible]

WI-3416	33 C T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTAGAGAGTC[C/T]CTCTTAGAGGTAGTTGTCTCGTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCCCAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACACATAATTAATCCCATTCCTAAAGAGACCAGG
WI-3453	70 C T	TTC TTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTAACAATAATGAAAAATCAGCTACTCTTTAGGCCCATCAGAG AAT[C/T]GAAGTCAATGGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	---	---	CATGCTAGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTAATTTAATGAGGTGGTGTGGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCAC[A/G]GTATTTTAATGAGGTGGTGTGGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGGTTTCT GGATGTCT	GGGTGACCCCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCATTAAGAAATGGTGAAAAATAAACCGGAGAGACCTGGG TTTCTGGATGTCT[C/T]TGAGGACAGGGTCAACCCAC
WI-3600b	146 G C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG TAAACATCT[G/C]ATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600a	78 T G	CCATGCCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTCAAGGTAATCCACTCACAATAGGCAATTGATGTATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGCTGTTATGATGCACCT[G/T]CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCAAAAGCCTTTATGTCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACACAAAAATATGACATAAAA T[A/C]AAAAAATACTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCATTCAGAAATACTCTCTGTCAATTTAACTTTGACTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAATGA AAAC	GGCTCACCAAT CATTTGTTTT	TCTAAAATGTGAAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAATGA AAAAC[T/C]JACACCGGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCCCCTTATTTAATGAAAA GATCTTGGGCAATTAACCTC

WI-1819	51 C T ---				GAAAAGCAGGAAGCCAGGACAGAACTTTTGAAGAGTCTTTTCAGCAC[C/T]TTCTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATCGGGTAACATGTTCCAGTGTTTTAACTTGACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAATGTGGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116 G A ---				GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTTCAATAGATAGACTAAGTAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49 T C CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAGACACAGT CATTAAAGTGAGAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25 A C G	TGACCAATGTC TTTAGAAGCA	TCGTGGGTGC CTCTCC		CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCGACGACACACAGGAAGGAGTGAG GTGAAGATGAAAGCAGTGTGACGAGCCACAAAGGTGAGGAAGCAAGGTTGCTGGCCACT
WI-3901	114 A G ---				GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTGCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCACCTGACAAAGTGG[A/G]TATCATGTGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99 C T GC	TGATTTCTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTTCTCTCAAGACTCACAGC[C/T]ACCATCCTTCACTTGTCTTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33 G A A	CCAAGAGGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCACTCCCAGGCCAAGAGCGTCTATGAATCAT[G/A]CATTGTTCTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84 A T	TTGAGGTCTTA GTGATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTTGTGTCATTTATTGCTTCTCTTATGTAAACACAATCACCACATTGAGG TCTTAGTCATTGTCATG[A/T]GTATAACAATATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117 A G	CCTATAATTTA GCAACAATAT CAACAGAA	TGCAGGTAGAA TTTTCTAATAT AGCC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTAGGTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGTCATCCCCCTGGATCTGAACGTTCTCATGATACT
WI-4168	32 A G AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATATACTTTCCAAATGACTAGTAGTAAGACGCTATTAATTTACCTATTATATT ATT/C/CATCATGATTTGCTGCCTTCTTCCAAATTTACTACAAATTGTATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACCTGGTCTGCCCTGT[C/T]GGTCTGTTCCTTTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGCAT
WI-4250b	117 A G	---	---	TAAAGTGCAATTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAGTGCTAAAGCAGTTTTTAACA GGTTCAATATGAGTCTGTGAACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCCTTCCAC	TAAAGTGCAATTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAGTGCTAAAGCAGTTTTTAACA GGTTCAATATGAGTCTGTGAACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	GGCCTACTTCA AGTTGTGTAAG G	TAAATGTCCTGGGAGATAATAGGAAAGTCCCATCCCTCTGTATACCTTGGTGTCTCCCCCATCACCT [G/C]CCTTACACAACCTTGAAGTAGGCCCATCCAAACACTGGTCAGAGAGTAATACTGTGCAC ACAGCCTCTTCAAATGGCACAATCAAAGCACCAAGTAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CATTGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
WI-4256	57 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGTCTTTTAAATGTACATGGCAGGACCGGAAATGG GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCCAGCCAC CCAGGACACTGCCATACT
WI-4325b	71 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGTCTTTTAAATGTACATGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCCAGCCAC CCAGGACACTGCCATACT
WI-4325a	58 C T	---	---	TGGCAGAAAGTCGGGTATGGCAAGTCAGGTGGTTAACTTGGATGCCACTTCTGCCTGTCACCTTCT CTAGACTCTTGACCCCTGCAGGAGGATCCCTGGCCTCCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCCTGTATCTGTTCAGGCC[C/A/G]GAATCGTCAACGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-4347	158 A G	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGCAAGTCTGGTGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGGACACACAAACAGTGGGACACAGGGGTACTTGTATACCTT/C]CTCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACTTGG
WI-1936	117 T C	---	---	AAAGAGGACTTTGACACACAACTTGG

WI-5204	54 C T	---			TAGATTTTGATGACAATAGGGAAGCCTTTGTTAAATTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G	CTCAAAA	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTCGC	TTTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATAATTTAACAGACTCAAAAA TAT[G/G]GCGAAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G	ATATAA	TTGTATCAAA GAGATGGGGT	AATTAAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGTGCTTTGCTTCTCCTCCAACTCTCTAGGGAACTTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTACTTTAAATTAACCTTGATCAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTCCACTGTCTATCAGTAA
WI-4456	49 C T	TATAGTTCC	AGTTGAATTA TTCAGAAAAAT	TTTCCTGTTAT GCATGAACCTTG	ACACATTTCAATTTGCTTTAAGTTGAATTAATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTTGGGCAATTGATTGAATTGT
WI-4461	49 A G	CTTCC	TCACTGTTATT TTAAAATTAT	TTTGACCTTTC ACCAATTTCA	CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCCTTCC[A/G]TGAAATTGGTGAAA GGTCAAGAATGAATCCACATTTTAGAATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75 G A	---		---	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGTATATAAAGAAACACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G	ACACGAAAGT	AAGCCAGACA	GGTGAAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAACAGTTAGTAAT CTTTCACCTTTTGATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160 T C	TAATC	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAA	GGGGTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATC[T/C]CTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G	ATGCTCTGAGT	CAGTGGTGAG	CCATGTCAGCA GCCTTG	GGGGTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C	AAGATG	CCAAGTAAGT CTATCATCTG	TTCTAAAAATA ACACTTCCCTGA AAAA	TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTGAATAATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTCTGGACAAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAATAATGGTGCCATAGTACTGGCTTCTGTGTGCAATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCAATGGCTGCATTTGTCCAGTC AAATGAGACAACCTTCCTAT
WI-4582	226	T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCTGTACACA AATAACTTTATGGGAGACAGCATTGTAAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT[C/C]CTCCTTGCTAGAAACCATTTGAT
WI-1965	105	G C	AG	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGCAACACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG[G/C]JAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C T	TTG	AGAAAAGAG AAGAAGGGAA AAA	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG[C/T]CTTTTGCTTTTTTTTCCCTTCTTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G C	CTACGTTGTT	TTTTAATTTTC TGGGTTGCT	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTA[G/C]JAGCAACCCAGAAAATTAACACGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTCTTTTCCCTTCTTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTGCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTCTGAAGCAGAAAAGCACTGTGA C[T/A]CATTTATTAGGCCCATCTCTGCTGAGCCCTGCTACAGCAATTTGTAAACATATGGCATTTGGG ACATATCTCTGAGCCCATCACTATTGACAAGATTCTCCTTTTAAACA
WI-5252	119	A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAAGTCTTGGGAAAAGGATTGTGATCATTTG AATCTGTTTAAATACAGAATTAATACTGAATACCTGTGTGAATCATTTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A G	CT	TGG	TGCAAAAAGGAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTCTTGTCAATTAAGTCTCTATTCA ATTACCATTTATCGGGGTAAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77	C A	GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG[C/A]CTTTTCATCTGCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCACCTCCTAGGTATGCACCCCTAAACATGGGTG GCAAT
WI-4649	50	C T	TTCCGAATG	TGTACTAGGTG TACTTACAAGA AATCATC	TCAGTGTTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAATCCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGTGATGTAATGTTGTGTAATTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGTCCAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAAATGATGATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTACCTGGCAATTTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTTGATGTGAGTGACATTTCTTTTGTGACGGAAGAAAACTTCAA C/GTTTCGAGAAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G	A	TGCACTATGG AACACACAC G	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGAGATTTATTTTC TGCACTATGGAACACACACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCAGCTTTGATGTTGAGATTTCAGAAAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAAACAGCAGTGTTGTCTAAAAAATATGATAGTTTCTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	TGTTTACGTTT CCTGTCTCATC GAA	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATTTGTGGCTTGCACAGGTGTTGTTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGCTCTTCAAGTTTACTACAGACCTCATCTCCTGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTOC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAAGTTATACAGGACCAGTGTGGAAATTTT AGCATTTCTGGGTTTGGCATCCATCAGGTTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGTGGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCCAGGCTCCTTCCACCATTTCTCCATCCTACTTCTACTCTGA[T/C] AGGCAGACTTATATGGAATAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGGCCCAAGA CCTCCTTCTCGGTTTCAGTGAAAAAGACGATGAACCTCTTCACTCTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACACCATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAAGAACATCTTCAATCACTCACCATTGTCTGTCTGTATTGTCCTTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACTGTGCTTTAAAGTGTGAAGTATTA ATTAGATTCTATTTTGATA[C/T]GATGTTTCTTTCAAGAGGAAATTTGTGTAAGAGGATTCCCAAT TGCAATTCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAATCTTCTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGTCTTATTTCTTTAGGAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAGATAACTAGAAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAAATCATCTTGCTAAGTTCC[A/G JTGAATAAAATATGCCAAATTTTAAATTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATT	CTACTCTTCT ATTTCTAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCCTTCATT[C/T]TTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAAGGTGAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCCA AGTCACTGACAGAGCCA
WI-4818b	121	G T	TGATAATGGG GCCCTGTT	CCTTCTTTTA TATGTATGCCA GA	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAACAATCTTATATA ATAATTTATTCAGAAGGAAATATACATATGGGGTGATAATGGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCTTCTTG AATAAAT	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCC[A/G]ACATGAATAACAATCTTAT ATAATAATTTATTCAGAAGGAAATATACATATGGGGTGATAATGGGGCCCTGTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTGTTTGATTCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAAGCAAGGTTAAT AATATAATAATATGATGTTATATATTACAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTTCTTTGCATCTATTCTAGGTTAATTCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAGATAACA	CAATCCACTA CCTCATTTAT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A G	---	---	AACATTTTTTAACCATGCTACATTTACAACACTGAAAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAACACGTGATACTGGAAGGAG
WI-4897	93	A G	---	---	GCCTTTTGTAGTTAAGTCTTTTGTAGTGTGCTTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAATAAGCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCT[G/A]CCTGCTATGGTTGCTTGTGAAGCCACATCCACT GAGGTATATCTGCTGCATTTTCTATATCAGTCTGAGTTTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143 T	C	AATAAGATGG TACCTTAACTA	CAAAGTTGGTA CAGAGAAATTC	AAA	TGCATGTTACTTCTTGGAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTACCCAAT CTTTTGAATAATTAACCTGTATCCCATCATGGTTCAATTTGCAAAAAATAAGATGGTACCTTAACCTA ATAAACAAATTCCTTGAAATCTCTGTACCAACCTTGCCTTTC
WI-9711b	423 T	A	---	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAACACAAAGAAACGCCTGGTGCAAGGCC CCAAATTCCTACTTCAATGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTAGTGTAGCTGTCTCGTATCCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C	A	---	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAACACAAAGAAACGCCTGGTGCAAGGCC CCAAATTCCTACTTCAATGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTAGTGTAGCTGTCTCGTATCCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G	A	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCTACTGCTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTTCACTTAACTTAACTGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCAGTGTCTACAGCATCTGATAG
WI-9702b	344 C	T	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCTACTGCTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTTCACTTAACTTAACTGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCAGTGTCTACAGCATCTGATAG
WI-9702a	179 C	T	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCTACTGCTATGATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTTCACTTAACTTAACTGATCTCTGTGA CTTTTATACTAGCTTTAAGAGGTTTTCATTCAGTGTCTACAGCATCTG
TIGR- A003N21	49 C	A	---	---	---	TATAGTATTTAACGAAGCCTAGAACGACGGCTGTGGGTGGTGGTTCAGTTCAGTCTACTCAGCCTGAGGTTGCAG ATATAATAACTTTGAAGCCATAACTTTTAACCTGGAGTGGTTGATTTCTTTTTTAAATTTTATTGGGA GGGTTTGGATTTAACTTTTTTAAATGTTGTTAAATAATTAAGTTTTTGTAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TIGR- A004V30	203 C	T	---	---	---	AGAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGCTAATTTTTAACATCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAATAAATTTATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAAAGTACAGTGATAAGAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGTC/G.TTCTTCTAGGTTAGTAGAAAAGTT

TGR- A004W22	232	C A ---			GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGCTGGGCAGTG CCCGAGGCGAGGAGGACAGTGGACAAGGATGCTCAGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCGATGGGAATGACCAAGTTCACACATCATGCACAGCAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTGGTGTCTGCCCGCCCTA[C/A]CTGGAGATGCTCTAAAA
TGR- A005D24 b	138	C T ---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCACAACATCTTTATAGAGAAAT[AG]AAACCCAA CT[C/T]TTTCAACCATTTAGTTGATTATCATCTGGAATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAAGGAAACAAT
TGR- A005D24 a	123	A G ---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCACAACATCTTTATAGAGAAAT[AG]AAACCCAA TTTCTCTTTCAACCATTTAGTTGATTATCATCTGGAATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAAGGAAACAAT
U03735	74	C G ---			TGAGTCTGAGCAGGATTGCAGCCAGGCCAGTGGGAGGGGCTGGCCAGTGCACCTCCGGGGCC GCATCC[C/G]TTAGTTCCACTGCCTCCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAAATGTTCTTTTAA
U39840b	42	T C ---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAAT[C]CAACAGCAAAACCCACA CAACCCAAACCGTCAACAGCATAATAAAATCCAACAACATTTTATTTTATTTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTCC
U39840	56	A C ---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAATCAACAGCAAAACAA[AC]ACCACA CAACCCAAACCGTCAACAGCATAATAAAATCCAACAACATTTTATTTTATTTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTCC
WI-8997	41	G A OCCC	GCCCACTTGCT	TGTTTGTACGC AGTGCTCA	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGCTCCCC[G/A]TGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACCAAGAACTGTGTCTCATGGT
WI-7008	180	A G ---			TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTACAGAA AGCACCCAGTTTCATGATAGGCAGTTTCAGGTTCATATGGTGACTTGATGACCCAGAGTCAAAACATTACAG TTTCCACCAAGCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG[AG]AGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26	C T	CGAATTTGCTG GGGAATCT	TCCCAAAAGTC TTAAGAAGAA AAA	GGTCCACGAATTTGCTGGGGAATCT[C/T]GTTTTTCTTCTTAAGACTTTTGGGACATGTTTGACTCC CGAATCACCAGCGTCTCTCTGTTTTCTGGTGG

WI-7593	46	G A ---	---	TTTTGTTTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAG[G/A]AATGAGATCAGTTTTGGGA CACTTCCTCTTGAATATAAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAA
WI-6962	78	A G ---	---	AGTGCACTTTGGGGAAAGGGCTCCAGTGTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAGA[G/G]GACAAAGCTCCTCAGTGAGCTGGTGATATCCAAAGACAGAACCCAAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATTTCCACAGCCTCACTTCATTTCCAC CTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
WI-7059	43	G G C C A A G G C A C C C A	GCTCCTCGCTG GGTCA	GCAGAGAGAGAACCATGCCAGGGGAGAGGACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAATATACCTGGGTGAAATATACCAAATTTCTGCATCTCCAGAGGAAATAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAAA
WI-9063	53	A C T T	TCTACTTTCTG CCCTTGGGT	AGCAGCCATCACATGATCTGTTTTTCCACCACTTCACTGAAGACACCACTTTAT[A/C]TACCCCAAGGG CAGAAAGTAGAACTTACTATTTCATTAATGTTTGACACAAATTGGAATTGTC
WI-7079	293	T G ---	---	AAGGGCATTGAGACTATAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAAGTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTTCTATTTCTTTTCCATTGCT TATTCTTGAGCACAAATGATAATCAATTATTACATTTATACATCACCTTTTGTGACTTTTCCAAGCCC TTTTACAGCTCTTGGCACTTTCTCGCCTAGGCCCTGTGAGGTAACTGGAT
WI-9074	38	A G A A A G	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAGTTCTTTTGTCTAAAGAA[G/A]AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249	C T ---	---	GGAGTTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGATGCCAGGAGACCCCTGAGGGCAGCCGGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCACGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCCTGCACCAGGTGGGGCCACAGCACAGCAGCATCTTTC[G/C]T
WI-7104	157	C A ---	---	GGAGTTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGATGCCAGGAGACCCCTGAGGGCAGCCGGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCCCTTGCAACCAGGTGGGGCCACAGCACAGCAGCATCTTTGCT
WI-8974	34	C T A A G A A C T C A	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTCAATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61	C T C C T G G C	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTTAGTTGCCCTAAGCATTGCCTGGC[C/T]TTC CTGTCTAGTCTCTCTGTAGGCCAAAGAAATGAACATTCCA
WI-9014c	93	T C ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCAGTCATCTTCTGTTCCAGAGAGGTGGGCTGGAT GTCTCCATCTCTGTCTCAACTTAT[C/G]TGCACTGAGCTGCAACTTCT

WI-9014b	44 C T ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTTTC/TTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGTCTCAACITTTATGTGCACGTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCCTCATGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGCTCCTACGGGTCCCC TCTTTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAACAC A/C/AIACACACATTTCTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCCTCATGGTTTGTGACAG(A/C)CCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGCTCCTACGGGTC CCCTCTTTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAA CACACACACATTTCTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTTGCCCTTCCCTC/TTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTAAATATTGTTGCCGCTGTGTGTTGTTGTTA
WI-9171	62 G A ---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGATTACAAAGACTTCATGC
WI-9174	47 T C T	CTAGACCCC ATTCTCCTATT	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATTTCTCTATTATTC/CAGTCCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGTCAAATTGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	AAGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAACACAGATAGATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCACAGACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGAACTACAGAGGACGATGTCCAAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTACAGACTTTCCTTTCATCTT
WI-9193	94 G A CA	AGAATATTGT CTGCCCTTAAAG	TTGGACAAACCTAGAAATTTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATTGTCTGCCCTTAAAGCA[G/A]TACCCCCCTACACACACACACCCCTGTCTC
WI-9015	48 C T ---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATTTGGGCTGGATTG[C/T]GCTTTGGTTAATACAT CTTTCCCTAAAGAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGCCAGGAGACAGCAGGTCTGAGAGAGGAGGCCAC[G/A]GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTCCCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGGAGCGAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G C	CAGGTCCCCA GATTGA	CACCTGCCAC ACTCAGAC	GTGACCCGTGAGGTCCGCCAGATTGA[G/C]GTCGTAGTGTGGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGCTGAGAGCAGGAGTTGAGGCCGAAGAAGTCA
WI-7836	120 T C C	CAAATAAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAATAGAGAGTTGAGATAAACACTCTCATTCACTAGTACTGAAAGAAACTCTGCTA GAATGATAAATGTATGTGTGCTATAACTCCAATAAACAATGCAACGTTCC[C/C]GATTTCTAAT CTGGTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCATACACAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAACTGACAG T A A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCCCTTTGGCCCTGCAGCATGTCATGCTCCAGAATTCAGCTTCAGCTTAACCTGACAGAT/C JGTTAAAGCTTTCTGGTTAGATTGTTTTCACCTTGGTGATCATGTCTTTCCATGTGTACCTGTAATATT TTCCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTTT TAAAT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAATCTTGAAATATCTCAAATGTTAATAACAATATGAATTTTTCTCATGCTACTATTACTACT AAGCATGTACGTGAATTTTAAAT[G/J]ATAGATGTAACTTTTAAATAAAATTTGGGGTGTGG
WI-7860	50 C G ---	A C G ---	---	GAAGATTAGGGAGGGTGTCTGTGGTCTCCTCCCTGCCCTCTCCCCA[C/A,G]TGGGAGAGAGCC TGTGATTTGCCAAGTCCCTGGACCCCTGGACCACTACTGGCCCTTATGGGTTGGGGTGTAGGCAGG TGAGCGTAAAGTGGGAGGGAAATGGTAAAGAGTCTACTCCAAACCTAGTCTCTATGTCAGACCCAG ACCTAGGTGCTTCTTAGGAGGGAAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 A G TTC	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGTA AGTCTCGCAGA	CAAGGCGTACCTCCAAACATAATTGATT[C/A,G]TATCTCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGGCCTGGCTACTGTCTCTCTGCACCTCTGCTGCTTG
WI-7307	128 G T ---	---	---	CACACTGTCTGTTCTTCAGTGTGAGGTCTCGCAGGTCCCTGGCAGGTGAGGTGGGTAAGCCGGGTTCCACA GGCCCCAGCCCTGGCAGGGTCTGCCCCCAGGTAGGCGGAGAGCAGTCCCTCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACTCATCTGAAGCCAGCTTGACACCTCCAGT TTGCACAGGGATTGTCTGCGGCTGAGGGCCCTGTCCCCACCCCGCC
WI-9274	25 C T G	GAAATGTGAC TTCACCTTGGT T G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTG[C/T]CAATGGACAGAAATTTCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACTTAATAGCTGGTTTTTACACCTTGATTTCGAGGTGGAA
WI-7313e	266 T C ---	---	---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAGTTCTTAAAT TGTTTTGCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 C T ---	---	---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAGTTCTTAAAT TGTTTTGCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTAACTGAATAGAAATGTATAGCGATGA

WI-9281	68	G A ---	---	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/A]TGTAGTTGCAGTCCTGTGTGCTTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A G CTC	CATTATTTTG AAAGCTATTCA GACA	TTCTGAAATATAACCAGCCATTGAGCTATTTAAACCTTGTAATTTTTTAATTTACAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAACATTAATGCTAACACTTTTTTAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAATAAATGTGAAATGGT
WI-9304	70	G A ACTGA	CCCCACAGAAC TATTGTAAAC AA	TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATTGCTTTGTATTGTATATTACATGATCACCGACT GA[G/A]AATATTGTTTTACAATAGTTCTGTGGGGCTGTTTTTTTGT
WI-7933b	314	C A ---	---	TTACAGAAACTTGCCCTGTGCTGTCCCATGCTAGGGCGGAGGGGTCTTTCTCTTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCCTCGTATCTACCTTCCCTTGTCCCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTTGGGAGGAACCATAGCTCCCT
WI-7933	96	G C ---	---	TTACAGAAACTTGCCCTGTGCTGTCCCATGCTAGGGCGGAGGGGTCTTTCTCTTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[C/C]CCTCGTATCCTACCTTCCCTTGTCCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGA CAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGAGGAACCATAGCT
WI-7374	182	T A ---	---	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAACTGAAA CCATGGTGAGAAAGTTTGACTTTTGTAAATATTTTGAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-9343	78	C T CCTCTGCCA	AAATGAAACTT ACGTTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCTTCCCAACAACAT CCCTCTGCCA[C/T]ACACAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104	T A ---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAAATTGT[A/T]A]GTGTTTGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G ---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTGTATTAT GCTCTTA[A/G]TGATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79	T C TTGG	CCTTAGAAAA TCTGCTTTAAC A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACACTTTAGAAAATCTG CTTTAACTTGG[T/C]ATTCTCTAATTGTGTTCCCTAGGAATGACTGTCCCAAG
WI-7423	107	T C GTTCC	GGTCCAGAAGA G000G	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCACCCCTTTGAGGAGGTGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCC[T/C]CGGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTTGGGTCTGGGAGGGTGGGTGAATAAAGGCATACTGTCT

WI-7424	131	T A A A A	CAAGAGAGAG AGAGGAAAGA	TGCAAGAAA GAATGAAAGTT G	CCAGGAGCTAGAGGGGAGGGAAGCAGAGTTAGAGAAAAAGCCACGGAGGAAAGG AAAAAACATCGCCAACTAGAAACGTTTTCATTCGTCTATCCAGAGAGAGGAAAGAAAA TT/AJACAACTTTCATTCCTTTCACGTTTCATAAACATTCACATA
X86400	118	A C ---		---	TCCTGCAAGAAGTTCTCAAGCCTTTTGGATTTTGTGCAATAAGTACAGCTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAAGCTTCTTCTAATTTAAGTGAGA/CJCTTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAATTTATGTACCACCTCGTTTATTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTCA
WI-8053	242	T A ---		---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAGAGTGTCCTCAATTAAGGGACTTTTAAATCAACCTAA TAACTCTAATTCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCAGTCTTAACCTTATATAA[T/A]TTCAGAAC
WI-6190	165	G A ---		---	TACACATGAATTGCTTTTATTCGGTATGCATCCACATTTTCAGCATTTAGTGGTCTGAACAGCAAG TGAAAGACGCGAGCAATTTGCCAGGAGGTCAAGCCCAATTTTCGGGATCTGCTGTGCACACCCGG GTTCCCTTCTTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCAGCAACCAAGGCATGCA CCGATTCAAGGTTCTTTTGTCCAGTTGTGAGATTCCTCAACTAGACCCCA
WI-6275	148	G C ---		---	AACAGTCAACCAACCATGACAACTCGCCAGGCAAGGCCCTGCTTCCCTCCCTTGGCTCCC ATGTGCCCTAGTCAGCAAGGTGCGGGAGGCAACCGATGTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA[G/C]GGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGCTGAA
WI-6421	41	G T ---		---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGT[G/T]GGGCTTCTGAAAGAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAAA GAATATTTGGGGCAGAACCTTGGAACCTGGCCACGAGGACATCCCAATATCCCTCTCTCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A ---		---	GGTGAGACGGGTTTATTGTGCACATTTACACAGCGTCACAGCGTGGGCTGGAGCGGCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCTTCACTTTTCTTCCACACACTATGTACAGTCACTGCTCCAA GGTGATGGGCTACAGTGTGCTGATCAGTGTGCTGTACACACATTTTACATAAATTACACAGCACTC ATACATGAAAAA[T/A]JAGAGCCTAAGGGCTGTATTTTATGAGAAAAAA
WI-9420	202	G A ---		---	AACTTGTTTACAAATAGGCTTTTGCAAACTTCATTACTGAATTGTAAAGTCAATGACTGTGTTTT TAAATATGTACCAAGGAATACAAATTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATTCCTTCTCACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGGAATACCTGGGAGAGAC TGCCTTGCCCATGGTTAAACCTACATAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTTAAGAAAAAATGGGCTTGTTCCCAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTCTAA TCTCTGGCTTGGATTTATCCAAAGCGCATGTTCTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAAGAGACACAGACAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCAAGATTCCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAAGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGT TTAATTAATTTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT[C]GCCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAATTTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAGTGATAAGGACAGGTCTAGAACAAGCGTTCCCAACCCCTGGCACCAATGACAGTTTGACCAAA TAACTCTTTGTTTCAGGGGACTGTCTACACATTTGTGGATGTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAACACCCCTCCCAACAATCATGACAATGAAAAATGCTTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGTT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCAACCCCACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGCACAGCCTAT TGGAAGAAATCATAAATGTAAACCCTACAATGTATTGCTCTCTGCTTGGTGCCAGGCATAGAGTT/G]GGCCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTCCCTTTTCTAAATGTTATGATTAATTAGTGCTTTTGTAAGAAATTTGAAAAAATGTAAA TCAGAGAAACAGAAAGAAATAAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGAA[G/A]AGGGAATGAGAAAAAGCACCAACCAAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48	A G ---	---	TGGTATTTTCTTCTAAATGTTATGATTAAATAGTGTCTTTGT[A/G]GAATTTGAAAAAATGT AAATCAGAGAAACAGAAAGAAATAAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAGACACACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAGGAAAGTTAAGT
WI-5696	61	C A ---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGACAATGTTCAAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAAACTGGGACCAAGATGACTTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153	C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTCTG TGGCAGGGACTGTGTCT[C/T]GTTCCCTGTTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221	G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTTGGTATACTTTCTCTTCTGAAGACCAACCCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCTACATCTGGAAACTAGATGAGTTAGGCTCTCTTTCATCT CAATTGAAATCTAGAA[G/A]AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAGTATCTACTCTCTTTAC[C/T]AAGTGTACTTTGCA TATATTTTATGGGATGATTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATTCATTTCCCT TTGTTTCAGGAGTTTCTTATTTGGCCTTCTTCTAAACCCCTTAACCATCTGCTTATTCCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A C ---	---	GAAACCTCGTTGGCTCAAAGGAAACTGTAG[A/C]AAATCTTTTTTTTATTTTGTGTTTTTAACTC AAAGAGTGGAGTTTGCAATGACCTTGATGATGCGACGCTGCTCTTTTGTGTTGGTGTAATCCCTTAGT GGCACCTTTGCAAAAGCAATTTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGTTGCTGAAAG TAGCAAATGGAAGAAAGGTTAATGGA
WI-10312	41	A G ---	---	AAGGCCAGTGGGAAAGCAGACAAACACTCCAAGAATAC[A/G]AGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGCGCATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGTGAGTCTTGCCCGAGTCCCATAGTAGGTGTTCCATAAATAAC AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179	C T ---	---	GATTCCTTTGCGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCAGGGGACTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAAGTGGGACAAAGGCTTGTCA[C/T]CTGTGCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGGTGAGGAGCTGAAGGCTGAAAGAATAGTCTCTGCTCTGGTCTTTGTTGAAATGGATGAGTCCTTTTACAAAATTTTCCCTCTTGCCATGGGTGTTATGTTTGAATCATGGAGTTGGAAGACTTAGATTCAATTTGGGCTGTACAGTTTACTGGAAGTTGTTA/GTTGAACCTTGAGCAAGTGCTCTTAAATGTCCTCTCA
WI-4701	198 G A ---	---	GGCTCAATGCCCTTCCCTGTAA GGGTTCAATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAATAAGGAAGAGATAGAAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACACATTTAACTCTCCCACTCTATACCGCCAAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A]CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCAATTTAATTAATTTGCACTTACTTGTGGCTACCAGACATTGCTTCCCAATTGTAAATTCCTTAACAACAGCAAGCATAAAGTGTGTCCTCATCTTTGTATTCCTAAAA[C/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGTCTTCTCTGTTCACCTCTGTATTTCCTATTTCAGCATTCAATGATTAA
WI-4860	72 A G ---	---	AAAAAACAACCTTCATTTGACATTTCTAAGAAGATAAAGAAAACAACGATCCACTGTGTGTTGCTTGATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAATTAACCAAAAGCAGTACACTAAAATAGCCTTTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCACTCTAACCTTCACATAGAGCATTAAATATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTTCAATGCCTACCAAGGTAAAGTAAATCGGAGGGGCGAGGAGTAGGAGTTGCTTCCGGATGTTGCATAAAATTCAGGTTCTTTAAGGAGTTGGCTGCC[C/A]AAAAATTTTAACACTGATGCTGTCTACAAACGCACATAGAAAATCGGTGTAGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATATGATTGTTGAATTTGTTGCTGTGTTCTTGGTG
TGR-A004Z48	177 A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTATGTAAGGGTGGGCGAGGGTGGACTGAAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCATCTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGAA/GTTCTCCAAATTTACAGGGGCTCCC GTGGGATGGTGGAGCCAAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCCAGAGACAGAATAGACCTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAGGACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGCTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTTCTGGCCTGCTTTTCGTTAACTGTGTATGTACATA TATATAATTTTAAATTTGAT[T/G]AAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAAGTTATTCTGTTTGTGTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTTGTAATAAAGTATATAATTTTTTATGTTTGTCTCTGA

WI-7747a	44	T C ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGC[T/C]TTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTTTGTTTGGTATCCTGCCAGTGTGTTGTTGTTAAAGAGATTGGAGCACTCTGA GTTTACCATTGTAATAAAGTATATAATTTTTTATGTTTGTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCCCTTTCAGCTCATTTTGCTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATTATTTCCCTTCAACAATAATAATTTTACAGAACGAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATATTAAAGCCTACAACATTTT[T/C]AG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCCAGCTGGACTCATGGATGTGACCCCTTTGCTCCCTGCTCTTTCTGCCCTCTGG[G/A]CTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCAAGGACCAAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGGAATGGAATGAATCAGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTTCTTCATCCCATCACCCCTAAATAGTCAAGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]JAGAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTCTGTTATTTTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCCTAATTTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATTTGTCAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGCAGCTGGATCACTTCCCGCAGTCCCTTGGGCAGCGCTTTGCTGTGGAACACGAGAGCTCCTCCT CAGGGCCTGGCAGTCACTCACCCTTCTATTCTGTATGATGATTTGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTGTTAATAATTGTAACCTTTATCCATTGAAAGTGTC AGCCATTTCAGATAAGCTATAATCTGGTCTTTAAGGAA[T/C]JACAACTTT
WI-7928	101	T G ---	---	CTCCCTTCCCTATGTCTCAGCAGCACGTTGGGCACACTTGTTCATCTTCTGACCCGTTTGTGGGCTA TTCCCTTGCAGTGCAGACATCGTCAAAATTCAT[T/G]JACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTTAAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTTTCGAGGTAAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAAGACTTAAAGGGCCCCAATGAATTTATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATTCTTTGGAGTTAAATGCACATATAGACACATACACCAACACTTACACCAAACT[A] ACTGAATGAAGAAGTATTTTGGTAACCGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGTTCCAGCCCGTTGCCCACTCATCTGCGGCTTTGCTTTTGGTTGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG[T/C]JAGCCCCAAAGTACAGCCTGGACCACTGCTGTG TGAGCTAGTAAGATTACCTGAGCTGAGCTGAGCCTGAGCCAAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATATTTTACACTCTTTGGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAATATGTGT[A/G]TTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTTCATTGTGGAATAGTTAACAGTCAAGGCTAACTGGTCAGTATTAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAAATGAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCTGTACTTACTTGCCCCCTTTTATCTTTCCCTCTTGCCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGGCAGTGTCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACACTCAAAAATTGGCAATGTCAATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATTGGATCCCCCAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTCCATTACGCCAGCTCATTGGCCAGAAAATTCAGGTGAGTGGCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCTATTGTCTATTGGCATTCCT[C/
WI-198	218 C T ---			GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCACC CATGATGGAAACTCTTGCCATGTTTTAGTACCCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAACTCTGCTAAAGACTAACCACTTCCCTATCTTATCTTCAGCTA CCTGCTTCCCCTT[C/T]GTTTAAACAAAGCATAGAAATATTCTGAACAAC
WI-205c	146 T C ---			TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG[T/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C ---			TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG[T/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCCAAGTNTTCCAGAGGTCTCAGACTACCTCCTCCATCTCCCCCT CTCCCCCACACACACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGCCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAAATCCAAAACACAT[A/G]CTTGACTCTCTTATCCTCCTCTTGTGTACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---			AGCTTTGAAATCCAAACCACATAG G CTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGAAAGACCTCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGCTTATCCTCCTGCTATCCTGATGACTGGGAAA
WI-427	59 G A ---			TTTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAAATTTAGAACTACTTCC G A GTTT TTCCCTGGGAAATATTCACAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCCTGACTCTGGCAGGATTAGCTACCACCTAGCTGTGAGACTTTATGT ATTCATTATTAGAGCCAGGGTCTTGCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAA T C AAATGGTCTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAA T C AAATGGTCTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTT C AATAAATGGTCTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG A G TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG A G TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT A G CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66	G C ---			TTCAAAATTTAACACCATGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTCTGACGTATTAACGTATTCGATCAGTCACCCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCTCACCCTACTTGGGCTCTGACTTCCCTTCTCTGGGCT GAACCTTCTCTGTGGCTGTCCGCTTCTCTGCTGGCTCCAATAC
WI-681b	156	A G ---			TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTGATGGTTT
WI-681	156	A G ---			TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACACAGATTATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAAATCTGTGATGGTTT
WI-867b	119	G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCTCTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-867	113	A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCTCTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-867	119	G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCTCTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-871b	123	C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCTGTATTGTACATAA
WI-871	123	C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCTGTATTGTACATAA

WI-884	198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAAATTGGGTCTGGAGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
WI-921b	205	G A ---	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCTCTCACGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGAACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205	G A ---	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCTCTCACGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGAACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACAGANGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTTCTTGCTTTA
WI-945b	90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACAGANGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTTCTTGCTTTA
WI-960b	167	C T ---	---	TTGCTTCAAAGAAGTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ---	---	TTGCTTCAAAGAAGTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTGCCTAGGTACATTTGTTTTATTGTCTG CGAATTGTTGTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTT CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCAGTAT[C/G]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 G A ---	---	---	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTTACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAAACCTTCTCTCTCCCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTTAGGATGAACCTTATCTGGCCAAACTGATA C[G/A]GTCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	---	GCATTCAGAGGGTTCGTTTAAATGACATTCACCTGAGGCCCTGTCTATGTACAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT TAAGTGCTGGGG[C/T]TCTGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	---	GCATTCAGAGGGTTCGTTTAAATGACATTCACCTGAGGCCCTGTCTATGTACAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTGCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN[T/C]GNCANT AAAAATGATTTGAAATTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 C T ---	---	---	TTCTCAATCCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	---	TTCTCAATCCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	---	TTCTCAATCCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGTCTNACAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	---	TTCTCAATCCCAATCTGTGTGTTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTTNGNNNTNG GGCTGGTGACTGTGCCTGGTCATTTAGAACCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTTAA/GJGC
WI-1306	240	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTTNGNNNTNG GGCTGGTGACTGTGCCTGGTCATTTAGAACCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAAAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJTCCTCTAGC
WI-1307b	118	T C ---	---	GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAA/T/CJGTGAGATTGTCTTT CCTACCCCTCTTAAATGTATCTTNCATTAATATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGCTGTGTTTCTCTCTGTAAGNTGTTT
WI-1307	118	T C ---	---	GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAA/T/CJGTGAGATTGTCTTT CCTACCCCTCTTAAATGTATCTTNCATTAATATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGCTGTGTTTCTCTCTGTAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCCTTTGCTCCTCT/T/CJACCCCTCAGAACTTCCCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCCTTTGCTCCTCT/T/CJACCCCTCAGAACTTCCCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAAGAGTCTGTTATTTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT/T/CJGAAAGTTGGTAGCTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAAGAGTCTGTTATTTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136	G A ---	---	TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGNNGNNTCCTTTCTNNTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTTNAATTATACCCAAGC [G/A]GGATTGTGATGGATCTGTTTATTTTCTGTGCTTGGACACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCGCCACCTTGCACTTAGCAAGTGT
WI-1349e	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCACAGGTCATAGAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCACAGGTCATAGAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCACAGGTCATAGAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCACAGGTCATAGAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCACAGGTCATAGAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57	C T ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58	T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGA TGCCACTTTATAAAGTTAGAGGTATTACCTTGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTCTTGCCCTGCATCATGCAITTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31	C T ---			CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTTGGAGGGCCCCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCCCTCGACTTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGGAGCGGTTGC AGCGAGGCCCTTAGGTCCGTATTTAATGTTTGTGTAAGAAAGTCGC
WI-1417b	31	C T ---			CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTTGGAGGGCCCCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCCCTCGACTTCGGAAGTTAAGGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGGAGCGGTTGC AGCGAGGCCCTTAGGTCCGTATTTAATGTTTGTGTAAGAAAGTCGC
WI-1729	172	A -- ---			CCATGAGCAACAGCATGTTTCTACTCTGTGTGTGTATGTTAGGGGCGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAGAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTTCCGTGGTACCTTCTCTCCACCACATCACCCTGIGTTTT
WI-1732b	122	T C ---			TGCCTTACTTCTTTGTTTCAATCCACCATTACATTTTGTAAATTGGAACCTTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTT/CJATTCACTCT CTGCCACATGTCTAGTAAGTGTGAGTGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114	C T ---			TGCCTTACTTCTTTGTTTCAATCCACCATTACATTTTGTAAATTGGAACCTTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTT/CJATTCACTCT CTGCCACATGTCTAGTAAGTGTGAGTGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97	A G ---			GCGAATTTAATGACTCCAAAGGTAGTAATCCTTCCCCCAAAAAGGTTTTAAATCTGTGTGGGA CATAATGTTTGAATTTGCAGTTACCTTGGI/GI/TTAAGGTGTGCTGTTTCTGGCAAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTCTTCCA
WI-1780	31	A G ---			GGTACACAAAGAAATGCTTCTGGAAATCTACI/GI/TAGCGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAAATGTGAACCAACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATTCTCATAGTTTACACATAGCTGGGAATCAGTCTGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAAGAATAATCATAAAAAAT
WI-1803c	77	A G ---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATIA/GIAGTAGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTACATATCCTG GGTGCTAATTTCAAAATATATCTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGAT[G]AGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA
WI-1837b	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC[C]TCTGTCCCCAGTTTATTTTTT AAGGTTTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1837	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC[C]TCTGTCCCCAGTTTATTTTTT AAGGTTTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G]GAGAACTCTGAATATTCAGCACATACAAAGTGTGACAAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAGTTCTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G]GAGAACTCTGAATATTCAGCACATACAAAGTGTGACAAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAGTTCTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCACCTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCCCTTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGGGTNAAGGACCTGCCNTTTTAC[C]TGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGTGCGACCCCTGTGCTTCT CAAGAAAAAAACAATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	GGGCTCACCTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCCCTTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGGGTNAAGGACCTGCCNTTTTAC[C]TGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGTGCGACCCCTGTGCTTCT CAAGAAAAAAACAATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCCCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C]TGTCTGTAGAGGT AAAGTCCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCATGAGAAACCACTTTTCTTGTCTCC

WI-1900	119 C T ---	---	TGTTCTGTGTCAGGCACCGGCTAAGTCTTGTCGATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAACCTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T ---	---	ATCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGTAGGGAAGAACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	ATCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGTAGGGAAGAACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	ATCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGTAGGGAAGAACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 A T ---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 T C ---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCAATTTCTTCATAGAGTNTTGTGTTTGTAGTCTCGTAATAATACTGTGGCCCTAGGAAGGTTGT TTTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATT[T /C]TAACAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102 T C ---	---	AAATTCTAGAAGCCAGAAGTCAGCTCACGATTTATAAAGTTGAAGTAAATGCAATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAACCTAGCTAAAAATC[T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAAGCACTCAAAAGTTATGTAGAGTAGCTGCTCTGAGTCACCTTTTTTCTACTCTCAIT GGCTTACCACATGCTTCCACTGGATC

WI-2013	127 C T ---			CTTTAGAGTGGTCAATTCGGTCCCTTCTGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTC/T]CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTCAGCTTCTGAGCCCTGGTACTGCAATCC
WI-2032c	166 G A ---			ACCAGACATCCCATCAGGAGTTAGTCCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAC[G/A]GTGGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCCGTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032b	219 C G ---			ACCAGACATCCCATCAGGAGTTAGTCCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/G]TTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032	219 C G ---			ACCAGACATCCCATCAGGAGTTAGTCCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/G]TTCCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2054b	188 C T ---			CGTTTCTTCTACATCTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACACAGAGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/C]TTCCTCTGCCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C ---			TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTCAAGGTTTCCGCTT/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCCTAGGTAGGGTAAGGCAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
WI-2573d	129 T C ---			TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTCAAGGTTTCCGCTTTCGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT/C]TTCCTAGGTAGGGTAAGGCAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
WI-2573c	165 A C ---			

WI-2573d	129	T C ---	---	TGGGATTAAACCCCTGTTTCTCCAGTTCAGTGGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTT[C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTATGCCTAGGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2573c	165	A C ---	---	TGGGATTAAACCCCTGTTTCTCCAGTTCAGTGGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTGTGATAT CATCTGATCTTCCCAACCAGGGCTTATT[C]TGCCTAGGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2573b	165	A C ---	---	TGGGATTAAACCCCTGTTTCTCCAGTTCAGTGGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTGTGATAT CATCTGATCTTCCCAACCAGGGCTTATT[C]TGCCTAGGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2573a	129	T C ---	---	TGGGATTAAACCCCTGTTTCTCCAGTTCAGTGGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTT[C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTATGCCTAGGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGACAAAGGTGCTATGGCTGGGCTTGGACGAG
WI-2868b	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAGAACAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAAAGCGCTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAGAACAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAAAGCGCTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C ---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTTAAATTATATCACAGCTTTATGTCCACTTCCCTGTTCCCTGCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C ---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTTAAATTATATCACAGCTTTATGTCCACTTCCCTGTTCCCTGCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	---	TTAGCACACATATCTGTTGGGACTTAAGTGAAGGATATAAAATTTA]CAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	---	TTAGCACACATATCTGTTGGGACTTAAGTGAAGGCA]G]TAAATAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	---	TTAGCACACATATCTGTTGGGACTTAAGTGAAGCA]G]TGATATAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACTCCTCCTCTTCTTAATAAACCTAAC ATTCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGTCCAGATTGCAATCCT AGTTCTTTAATGTTATTCGAAAGAAACCTTTTACTTAGGGATTGTCT
WI-2971	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACTCCTCCTCTTCTTAATAAACCTAAC ATTCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGTCCAGATTGCAATCCT AGTTCTTTAATGTTATTCGAAAGAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTT]A /T]AAATCTTTCTTTCTGGTGT]T]AAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTT]A AATCTTTCTTTCTGGT]G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTT]A /T]AAATCTTTCTTTCTGGTGT]T]AAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-3292b	106	G A ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTTCATTAATGTATTAATTAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAATGGAAAACATTCATGGAAAAAACCCATTTCATC
WI-3292	106	G A ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTTCATTAATGTATTAATTAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAAATGGAAAACATTCATGGAAAAAACCCATTTCATC
WI-3355	19	G C ---	---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAACTTCAGAGTCCCTCTTACTGGAGAGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATATCTTCCCAAGCACTTAAACTCATCAGAA AAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---	---	CCATGAAGATGAGTTCCCTCCCTCCCTGGTCAAGTCTAAGAATAGCACACCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTNAGCTTT CTGGAATTGGGATGAATCTNACATTCATCAATGTGCACCTTCGTGTGGATCATTCTOC[G/A]TGCCCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	---	---	TAACCTATGCCCTCATCTGGCTTACTGCTTAGTTCCTTGTGTCATCAGTGCACCTTAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAATTGGGAAAATATGTTTGCATAT
WI-3505	131	G A ---	---	---	TAACCTATGCCCTCATCTGGCTTACTGCTTAGTTCCTTGTGTCATCAGTGCACCTTAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAATTGGGAAAATATGTTTGCATAT
WI-3564b	177	C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACCTGTTGACTAACGTTAACATGCTGTCTGTT[C/T]AACAAAGTGTGTTGTGGTGTATC AGTGTACACATGCTACCTTCTTCACAAACAAA
WI-3564	177	C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACCTGTTGACTAACGTTAACATGCTGTCTGTT[C/T]AACAAAGTGTGTTGTGGTGTATC AGTGTACACATGCTACCTTCTTCACAAACAAA

WI-3649	64 A G ---	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGAAGATTACAC[A/G] AGACCAAGTTTGCCTTCACTTAGTAGGGCCAATGATAGACTTTTTAGGTGCTACCAACAAGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCCTGCCCTTGGTC TTCCTGTTTTACCATAATTAATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAAGCGGAGTGCTTTTATAGTAATTAATAATATGTTTATTTAGAAAATAACAAAAT[G /C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTTGGTCAAAATGATTGTT AATTCTTAATTAATTGTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133 G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAAGCGGAGTGCTTTTATAGTAATTAATAATATGTTTATTTAGAAAATAACAAAAT[G /C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTTGGTCAAAATGATTGTT AATTCTTAATTAATTGTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137 G A ---	---	CAATATAGACCAATGACTGCCACAAGAGAAAATTAGTGGATCTACATTTAGAAAACCACATGTTTTT ATTGGCTCTCTCTCTCTCTCTTTTAAATGCTCTCTCCAACACCAATTCACTTTATCTTTTCAA T[G/A]AGCATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTTCACAAGTATACATTA GCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGG CAAAGACCAAGGACAACCTGTAGGACTTCTGCACTGGTCTACCTCCTCCTAGGCTTCTTGATTAATACTC TGTTTCAGGAAGGCAAGGCGAGTTATGACCACTTACAACTGAGGAAATCAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194 G A ---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGG CAAAGACCAAGGACAACCTGTAGGACTTCTGCACTGGTCTACCTCCTCCTAGGCTTCTTGATTAATACTC TGTTTCAGGAAGGCAAGGCGAGTTATGACCACTTACAACTGAGGAAATCAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210 G A ---	---	AGCCAGCCACATCATGTTGAGTCCCTGCTCATTCTCCATCTCTTATTTCTCTCTACTGCCCTTCACTT CCATTAAACAAGAACTCTTGATTACATTGTATGTTGTGGTTACACTACAGAAATCCAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATTCATTTTGCAATCTTTGTCAATTAACATAATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130 T C ---	---	GAAAAATGATGTTTTTGATTTCCCTTCCCTATCTTCAGATTATTGGAGTGTATTAGAAAAGTATAGT AACCTTTTATTGATGAACCTCTGTCTATAATTAACCTTCCCTCTCTCTGCTTTATTTTGGCTT[C]ACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAGTAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTNGGGGTTTTTCTGGGAAGA

WI-4110	130	T C ---			GAAAAATGATGTTTTGATTTCCTTCCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTGATGAACCTCTGTCTATAATTAAACCTTCCTCTCTCTGCTTTATTTTGCCCTTC/CJACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGNGGGGTTTTCTCTGGGAAGA
WI-4119b	168	G A ---			ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTAAAGGGCTCTGTGTGATCATCACTTCA
WI-4119	168	G A ---			ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTAAAGGGCTCTGTGTGATCATCACTTCA
WI-4123b	51	T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTTGAAATAGAAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAAATTGTATAGAATTTAGTGGGG TTCTCCATGACATTGGCTTGTCTTCTCTCAACAGTGGGTGGTGGATGTTTTCCATGCTTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTTGAAATAGAAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAAATTGTATAGAATTTAGTGGGG TTCTCCATGACATTGGCTTGTCTTCTCTCAACAGTGGGTGGTGGATGTTTTCCATGCTTTCTC AGGCACAAACACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C ---			TTGTACATGTTTCATTCATCCCTCCCATCTTTTCTGTCTTATAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---			TTGTACATGTTTCATTCATCCCTCCCATCTTTTCTGTCTTATAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT T/C]GTGCTGTGCTTGTGAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	G A ---			TACACACTTTTTCATTTGGTTTCTTACTGCAGTTAAAGGACCATCCATTATATTACAATCCCTC AGTTCTATGCTTTAGAGTNCCTATTATAGGACTACTGTAAATTTTCAGAGGGAATTACTCCTGGAGTA GGGGAATGAGTTAAATAATCTACACATGCCAATTGCAGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG

WI-4230	93 T ---			AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAACATTTGATAAGAAATGATGAAA GTTTGTCACATTCAGATTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACT TTTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTTCTGAAT ACATTTTAAATGGAGGAGAAATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C T ---			GAAATTCATTGAAGTTTGGACCTTGAACCTGATCTCATTAAATACATTTTNCCTTGTAGTGGTTGTAATTT CATTTTGGACAAACAGAACAGAGAAATTTCCACTTAAATTAATTAATTCCTC[CT]AAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTTATCTCCTAGATATTTCTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A ---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTACAGGGAGCCCCAACCCCTTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTACAGGGAGCCCCAACCCCTTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---			AATCGAAACATTGATTTTTTTGTAAAGGAACCACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAAGCGGTAA
WI-4389	156 G A ---			AATCGAAACATTGATTTTTTTGTAAAGGAACCACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAAGCGGTAA
WI-4488	31 A G ---			GATGACAATTATTGTGATTGGCATTTTAA[A/G]GTACCATTCATTTCTTCTGGCTTTCGTTGTT TGTTGTTGAGAAGTCAGGGTTAGTCGTATTGCTCCTTTTCTAGTTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---			ACCATCAATGTATCACCTTCTAAAAATTTTAGATGATTAACTGGCTCTGTTAAAAAATAAAACCT GCTTTGGACATTGAAAAATAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACCTA AACAAAGTTAAG[G/C]JGTTTTTGGAGGGGAAAAATCATAAAATGCATAAAATTTCTACCACCTGTCA TTTCTTGTCCTATAAATAAAATTTTACATGCCT

WI-4584	144 A G ---	---	TTGGTTGGCATTATAGCCTCATAACAACATAATTTACAATCATAATTGTTACTCTTATTTACAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCAGAGCCCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAATAATGTTTAAATTAATCTATGCAATAGATTTCAAAAGA GTCCTAATGTGGTTTGAAATAGGTGCTTAAATTTGTTTATCAGTATGC
WI-4639	185 C T ---	---	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAATCCACCATTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTTAAGGACACCTATCATAGTAATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA[A/-]GATTACTCATAAAAGCATATTAATTTTATAAATATGGAATAATTAAGTAAATGTGAAT TGAGTTTGAAGGTGTCATGAGAGTAGGGAGGAGTAGTTTCTACTTATAGGGTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAATGATGAACGTGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	GCCTTTGAGAAATGAAAAGGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTGTGTAT TTATTGTTTACATTATTAAT[C/T]GTCTGTCTCCCTTCTGGTATGCTTGTGTCATGAACAATGAATTC CCCAGTGCCCTGCCGATGCTGGCTCCTAGAGGTGTCAGAGAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTCAGAAATTGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAACACATTATTTAATTT[G/A]AAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTTCCCTTCTCAGCAGTTTCCATGTCGTGATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCAACAA
WI-5404	87 G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAACACATTATTTAATTT[G/A]AAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTTCCCTTCTCAGCAGTTTCCATGTCGTGATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCAACAA
WI-5545b	77 A C ---	---	TAGGAAAGGGGATGGTGAATGGCCTCTGAGACATTTAAATCTATTTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA
WI-5545	77 A C ---	---	TAGGAAAGGGGATGGTGAATGGCCTCTGAGACATTTAAATCTATTTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA

WI-5860b	134	A G ---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC[AV GJTATACCTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC[AV GJTATACCTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATTCCACCCAGGTCTACTACATTAAATCAACCCTAACCCACAATAC TATATATTGTCCTGTTCTGAATTATTTTCAATTTAGAACTGTAGATTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCCTATATTNCTGTTCTGTGCATACCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTGTT[C]CTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTGTT[C]CTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T C ---	---	AAGATAGACAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCCTATATTNCTGTTCTGTGCATACCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6112	96	T C ---	---	AATGCCTATCACCTTCCATCATGCTGCATAAATGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[T/C]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTTGACTAAACACATACCTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103	T C ---	---	TAATTGCACAACTTACATATCAGGGTTTCTGATTGAAAGGAAGAGAATAATTCCTTTTAGTGATT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTTC/C/GCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGAAGACTT CCTATTTCTTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T ---	---	CTGGCCTTATAATCCAAGTTTAGGATTAAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAAGATTTCCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTC/C/TACTCTCCCT GGTCTTATTGACTTTTCAGGGAGCCTAGAAGAGCTGGACAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTTACGATTTTTTA
WI-6336b	234	C T ---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGCTTGGTAGAGCC/C/TJTGAGGACACTGACAGT
WI-6336	234	C T ---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGCTTGGTAGAGCC/C/TJTGAGGACACTGACAGT
WI-6381	92	C A ---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTTAACAA/C/A/GTATTTTAAAGCTCAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G ---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTGAGGCAGTAGAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAAAGGCTTAGGAAGACAGTAGTCTCTGTGTTGAA ATTTTGGTGTCAATAATAAGAAGTTTAGACTTTTGGTGGTTGTAGTAGTTGTAGTAGGAGCGTT/C/ GJATTGGGTGTTATCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTGT
WI-6449	186	C T ---	---	GAGGCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGTCTCACACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGTTCTATTATCTGCAATTCCTGATCTTATGTCTGGCTCTATT/C/TJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAITTTTCTGTGGTGTATTATA
WI-6449	186	C T ---	---	GAGGCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTCTGATTGGTTGGTGTCTCACACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGTTCTATTATCTGCAATTCCTGATCTTATGTCTGGCTCTATT/C/TJATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAITTTTCTGTGGTGTATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACAT/C/TGAAAAAAATTAAGTAGAACTCAAAGAGCCAAAAAGTCCCAATTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTCTCCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA[C/T]GTTGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA[C/T]GTTGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACTCAATTAACTTTGCAACACTGAGAAAAATCGGATTTGGAGATCTGCAAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCCCAATAGTGGAGAAATCAGAGT/AJGCTCCTTGTGCTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACTCAATTAACTTTGCAACACTGAGAAAAATCGGATTTGGAGATCTGCAAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCCCAATAGTGGAGAAATCAGAGT/AJGCTCCTTGTGCTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAGAGAACACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGTCTGTGTAAAG GTTCCCTTGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGTCTGTGTAAAG GTTCCCTTGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCCTAGTCTCCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTCCAGCACCTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCAGGCACACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCCTAGTCTCCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTCCAGCACCTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCAGGCACACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6666	68 C	A	---	GTTAGACAGTATCCAGCAAAAGGTTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCCTACTCTGTTGGTTTCATGTAA ATGTTTGGGGTGACTCATTCGGCTCTCTCTCTCAAGTTCCAGGCTTCTTGGGTAGACCAAACTA ATACACAATGTTAGGCACACAAGAGA
WI-6670b	120 A	G	---	AGATTAAACATAATTATCTGGGGCCATTGTAGGGTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTCAGGGCCGGAGTCAGGGTTTGIGGGCCAGAGTTTAGACAATTTGGGGAATTCCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6670	120 A	G	---	AGATTAAACATAATTATCTGGGGCCATTGTAGGGTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTCAGGGCCGGAGTCAGGGTTTGIGGGCCAGAGTTTAGACAATTTGGGGAATTCCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6704c	33 T	C	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACAIG
WI-6704b	33 T	C	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACAIG
WI-6704	28 T	C	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAAC[T/C]AACCTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACAIG

WI-6710	106	G A ---	---	CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTTAAACACATTTTGTACGGCTGGAATGATCCC[G/A]TAGTAAAACTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGACTATTTACTAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCTGACAGGAAAGGTC
WI-6766b	148	G C ---	---	AAACAAATGGTGCATTGCATAATATTTGTGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6766	148	G C ---	---	AAACAAATGGTGCATTGCATAATATTTGTGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6787b	97	A G ---	---	ACAGATAAAAGTCTTTATCCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAATTTACAG[A/G]TTTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105	C G ---	---	GAACCCACGAGTCTGTTATTTTATTAAAGGAGCATTTACATTATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAATCAGTCAACCC[C/G]GAGTTAGAAAGTAGATCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCCGGAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37	T C ---	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTTA[T/C]JAGAAGCATTTTTAATTTTACAACACA AAGCTCAAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGTCTATGNACAAAGTACAAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGGGCAATGAAGTTAAT
WI-6810	37	T C ---	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTTA[T/C]JAGAAGCATTTTTAATTTTACAACACA AAGCTCAAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGTCTATGNACAAAGTACAAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGGGCAATGAAGTTAAT
WI-6817b	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]JTGTGGATACCCCTGTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAAACCAAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACTCAACATGTAGCT GCAGGGTAAAC[C/A]TGTGGATACCCCTGTGTCTCTACTNGCCTCCAAAGGCATTTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAAGTGGGCTGTGCAG
WI-6819b	221	C ---	---	GATGGAAGCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATTTTG CTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGGAAGCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTAT TTGCTTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAGCTTTATTGGCTCCAACAAATTATCCCTTTTAAACTCCTCTTCTTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAGCTTTATTGGCTCCAACAAATTATCCCTTTTAAACTCCTCTTCTTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTGAACAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACATAAGTAAATACAGCAGATGAGATGTCTCTCACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTTCAGTGTAAATTCACAAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGGCATACGNGTAAATGAAGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCCTGAATCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTTGCAGGCAAACTTC[G/A]TAGAGCCATTCTGTGCAGAAGAGGGAAGGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGCGCTGTAGAACTGAGCTCATTA
WI-6909	73	C T ---	---	ATTGAAAACCTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGATGC AGACTT[C/T]AAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAAATTTCCCTTTTGGCCAACAGGATTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163	G T ---	---	CACTCAAAACCTTTATTGATTGATTTACAAACTGTACAATAATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]GAGATGTAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAAGTCCCGACCTTCCATGTGAATGACTCTTCCCTTGGC
WI-6915	144	A ---	---	GCTTGTTTTTTTTGTTTTTTAAGTGACACCTTGGCCTTGTGGCAATTTCTTCACTTATCTTACCC AAAGTGCCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGGTAGTATTTTTCAGATTTCCACAAAGAACATG TATTGCTTTTGTAATTTGAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C ---	---	CAATCAAAAGTTCAAAGTTTCAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTCTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAAGTTCACTCTTAATTTCAATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C ---	---	CAATCAAAAGTTCAAAGTTTCAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTCTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAAGTTCACTCTTAATTTCAATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A ---	---	TTTTATGAACATTTTCAGATTCCCTCATATCAGCAGCATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATCCCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATTAAANCAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	G A ---	---	TTTTATGAACATTTTCAGATTCCCTCATATCAGCAGCATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATCCCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATTAAANCAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47	C G ---	---	AAACTAAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCCTACTTAAGAAGCATTCCAGTCAATAATACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAAACCACTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6996c	242	G T ---	---	ACTTCTAGTGCCTCTGTTACCACCCTCTAATGCCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCCTGGCTCCCTCCCTCTGTCTTCAGCACCCAGAGGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGACT CTCTCCTGATGTGGGCCCTCTGTGCTCTTCTCTTCC[G/T]GTCCGATC

[illegible]

WI-7175	194	C T ---	---	CTCTAGACTAGTGCTTTACCTTTATTAATGAAGTGTGACAGGAAGCCCAAGGAGTGTCTCACC ATACTTCAGAGAAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGTTTACTGCTGTCATGTCATGCCATA[C/T]AGAT AATTTATTTTGTTATTTTGAATAAAACATTTGTACATTTCCCTGATACTGGG
WI-7178b	273	G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAAGTGTCTGGCTTTTCCCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTGCTGCACTAAGAGAAATTTGCACCTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7178	273	G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAAGTGTCTGGCTTTTCCCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTGCTGCACTAAGAGAAATTTGCACCTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7182b	116	A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCACTCTGAGCCT[A/C]TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7182	106	C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCACTCTGAGCCT[A/C]TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7191b	273	T A ---	---	ATAATTGCTTGTCTTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCAACACACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGAATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCATTT
WI-7199c	112	T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGACCTCCTTGACCTATGAGC[T/C]GGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTGCTCTGAATTTCTCTTTATTAT AGTCCATAGTTTTACTCCTCAGTTCCCTCACCATCATCATCTTGCTAA
WI-7199b	112	T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGACCTCCTTGACCTATGAGC[T/C]GGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTGCTCTGAATTTCTCTTTATTAT AGTCCATAGTTTTACTCCTCAGTTCCCTCACCATCATCATCTTGCTAA

WI-7216c	237	T C ---				TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTGTTT[C]TGTGTAATCACTT
WI-7216b	237	T C ---				TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTGTTT[C]TGTGTAATCACTT
WI-7220b	147	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCAACCATTAATTTGTCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[AT]AATCTTGAGCACAGTGAATGACCTATCCTGCAACACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTTT
WI-7220	140	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCAACCATTAATTTGTCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC[AT]CTAGAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTTT
WI-7226	232	C ---				GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGTAATTTGTAAATAGTGACATATATGTATA TACATATCACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATT CCCTTTTCCATATAGGAAACATAAATTTGAAGTGGCCAGATGAGTTTATCATGTGCAGTGAAAAATAA TTACCCACAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTT
WI-7228b	254	G A ---				ATAGCTTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTCATAA TATGTTCAACCAGGAGATTACAATTTTGTCTCTCTTGTCTTTGTAACTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAATGTTATCCAACCTATTAAGATAATCTCAATGT
WI-7228a	163	G A ---				ATAGCTTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTCATAA TATGTTCAACCAGGAGATTACAATTTTGTCTCTCTTGTCTTTGTAACTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGGATCAGAA[G]AATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAATGTTATCCAACCTATTAAGATAATCTCAA
WI-7233c	213	C T ---				CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCTGGTCTTGTGTACATTCATTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACTAATTATATTTAAATTTATTTCTAGGAAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTTCCACCTTTTGTGGCAATATTAAAGTGAAGTGCCTAATA GTGTAAGTA[C]TGTGACAAAACCACTGCCAGATAACCAAGAGGGGCTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTGTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATTATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTGACACCTTTTGTGGCAATATTAAAGTGAAGTCTGCTAATA GTGTAAGTAC/TJGTGCACAAACCACTGCCAGATAACCAGAGGGCCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTGTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATTATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTGACACCTTTTGTGGCAATATTAAAGTGAAGTCTGCTAATA GTGTAAGT/CJACGTGCACAAACCACTGCCAGATAACCAGAGGGCCTG
WI-7238	128	T C	---	GCGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTTT/CJCCGTT CTGTTTTAAACAGAAAAATAAAGGAGGTGAAGCTCCTTTCTCATTTTCAAAAGTTGCTACCCAGTGTAT GCAGTAATTAGAACAAAGAAGAACATTAGTAGAACATTTTATTGCTA
WI-7252f	520	T C	---	CCACGAGGATCCCAGCCCAAGGGCCCTCCCGCCCTTCCACTCGCAGCAGCCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCCTGGCTCGGAGGCTGCCCGCCCTGGTCTCTGTTCTGTCG GACACTCCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252e	552	T C	---	CCACGAGGATCCCAGCCCAAGGGCCCTCCCGCCCTTCCACTCGCAGCAGCCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCCTGGCTCGGAGGCTGCCCGCCCTGGTCTCTGTTCTGTCG GACACTCCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252d	540	T C	---	CCACGAGGATCCCAGCCCAAGGGCCCTCCCGCCCTTCCACTCGCAGCAGCCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCCTGGCTCGGAGGCTGCCCGCCCTGGTCTCTGTTCTGTCG GACACTCCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252c	552	T C	---	CCACGAGGATCCCAGCCCAAGGGCCCTCCCGCCCTTCCACTCGCAGCAGCCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCCTGGCTCGGAGGCTGCCCGCCCTGGTCTCTGTTCTGTCG GACACTCCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252b	540	T C	---	CCACGAGGATCCCAGCCCAAGGGCCCTCCCGCCCTTCCACTCGCAGCAGCCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGCCCTGGCTCGGAGGCTGCCCGCCCTGGTCTCTGTTCTGTCG GACACTCCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA

WI-7252a	520	T C ---	---	CCACCAGGATCCAGCCCAAGCGGCCCTCCCGCCCTCCACTCGCAGCAGCGCGGGACAGAG GCCTGCCGGGGGCGCAGCCCCGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCGAGCCCTAGAGCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCTTT/
WI-7265l	231	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265k	121	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTA GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265j	174	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265i	227	T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265h	80	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTA GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265g	170	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCATTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTTGCCT

WI-7301	205	A C ---	---	AACTATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACIATGGTGGTGGTGGAACTATAATGATTTGGAAATTACAGTGGACAAACAGCAATCA AATTIAC]JGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49	G A ---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/A]TTGTTCTACCTCAGT AGAGGGAACAGAGGATATTGCTTCCTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314b	49	G A ---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/A]TTGTTCTACCTCAGT AGAGGGAACAGAGGATATTGCTTCCTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314	36	A G ---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAA[G/TT]TTGGGAGGTCAAGTTGTTCTACCTCAGT AGAGGGAACAGAGGATATTGCTTCCTTTGCAGCAGTGTAAATAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7321b	199	C T ---	---	ACTCAGGGAAGGATGCCCATTAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAAATCAAGNNNNNNNAGGGTGGCACACCCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	ACTCAGGGAAGGATGCCCATTAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAAATCAAGNNNNNNNAGGGTGGCACACCCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C ---	---	AGACATTCTCGCTCCCTGAAAGACTGAAGAAAGTGTAGTGATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCTCAGGCTACTATAGTCCAGAGTCCCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATAATTCTGAATTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7338c	221	A G ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAATTCGT

WI-7338b	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCTGTT
WI-7338	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCTGTT
WI-7338	221	A G ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCTGTT
WI-7384c	146	T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAATACCATTAATACATTTGTATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATTTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146	T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAATACCATTAATACATTTGTATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATTTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145	T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAATACCATTAATACATTTGTATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATTTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7388c	106	A T ---	---	TGAAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTTATTTTACTTTGCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCCTCTATTTTGGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCTGCAAGAATTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7388b	106	A T ---	---	TGAAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTTATTTTACTTTGCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCCTCTATTTTGGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCTGCAAGAATTTTCCCCCAAGATGTGTATAGTTATTGG

WI-7388	94 T A ---			TGAAATCCTGGGTCTCTTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGTTACCTCTATTTTGGCCACAAGCGTCTCGGATTGTGTTTGA CTTGTGCTGTCCAAGAACTTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7438	64 A G ---			TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCTCTGG[A/G] GTTGATATGACAAGGAAACCCTATTGGAAACCAAGTCTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTACATAGTTTGTCGTTGTTGTTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---			CCATGATCCCCCTCCTCTTGCCAAATGGAGGAGCCCTGTGGATGGTACCAACAACAGCCCAAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7454	152 T C ---			CCATGATCCCCCTCCTCTTGCCAAATGGAGGAGCCCTGTGGATGGTACCAACAACAGCCCAAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177 G C ---			AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACCTCAGTCCATCTTAACCATGTACAAATGCACATAAATTACTATTTATAATTCTATGTA CAACAGAGCCACAGCAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAACGTTTACCAACAATTAT
WI-7464b	168 C A ---			AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACCTCAGTCCATCTTAACCATGTACAAATGCACATAAATTACTATTTATAATTCTATGTA CAACAGAGCCACAGCAAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAACGTTTACCAACAATTAT
WI-7464a	103 C A ---			AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACCTCAGTCCATCTTAACCATGTACAAATG[C/A]ACTAAATTACTATTTATAATTCTAT GTACAACAGAGCCACAGCAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAACGTTTACCAACAATTAT
WI-7499b	134 T G ---			CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATTCAGACAAACTTCCACTTCGAAGGTTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCA[T /G]TATAGTCCCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAATCCCTTTGAAAATATAAATTTGGAAATGAGTGAIGA

WI-7499a	33	A G ---			CAATTCTCAATCCAACCTAGTCTGINTGCCTAAJAGJCCATTCCAGACAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTITTAGGAA CTCTGTACAAAATTCCTTTTGAAATATAAAATTTTGAAATGAGTGATGA
WI-7506b	118	A C ---			TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGTAGTCTGTGCTGATTGCCTAGC[AC]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAATAATCATGATGTCATGATGCAGTAATTAATGATCA GAAGAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A C ---			TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGTAGTCTGTGCTGATTGCCTAGC[AC]GGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAATAATCATGATGTCATGATGCAGTAATTAATGATCA GAAGAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C T ---			TGTGAATTCCTTAGCTCTGGAAGGTGTTTATGCCCTTGGGGTTTCTTGATGTGTCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATTCGGGTGATAGAATTGCT AAATTGT[C/T]GTGAAATAGGTTAGAAATTTTCTTAAATATGGTTTCTTATTCGTGAAAATTCGG AGAGTGTCTGCTAAAATTGGATTGGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135	T C ---			TGTGAATTCCTTAGCTCTGGAAGGTGTTTATGCCCTTGGGGTTTCTTGATGTGTCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATTCGGGTGATAGAATTGCT /CJAAATTGTCTGTAATAGGTTAGAAATTTTCTTAAATATGGTTTCTTATTCGTGAAAATTCGG AGAGTGTCTGCTAAAATTGGATTGGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G A ---			GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCCCTCTTTCCTTTG[A]GGAAGACCAGCTTTCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGCTGCTCTGGCTCTGGATGTAGTCAGTTA
WI-7543	162	G A ---			GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCCCTCTTTCCTTTG[A]GGAAGACCAGCTTTCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGCTGCTCTGGCTCTGGATGTAGTCAGTTA
WI-7555c	60	T C ---			GGTGATCAAGATCTGTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJCTA AAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTGCTGCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAATAATGAAGTCTGACTAGAAATTCATTTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCAATTTTGAATTCAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJCTA AAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCCTGCAATTCCTGTTAAAGCCACTTGGTG ATAAGAAGGGAAGTAAATAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTICAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTT/CJCTA AAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCCTGCAATTCCTGTTAAAGCCACTTGGTG ATAAGAAGGGAAGTAAATAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTICAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAAAGAAAGCCCAATTTTCAACTGCTTTGAAACTTGCCCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCCTTGG ATCGCTAAGCTGGCTCTGTTTGTGATGCTATTTATGCAAGTTAGGCTCTATGTAATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCCCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T C ---	---	AATGTATCCCTTTCGGTCCAAACACAGGAACCTGACTGGGCGAGTGAAGGAAGGATGGCA[T/C] AGCGTTATGTGTAAATAACAAGTATCTGTATGACACCCGGGATCGTTTGCAAGTAACTGAATCCAT TGCGACATTTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTTGATGAGTTCCACTTGATCATGCGCTACCCGAGGAGGAAGAGTTTG
WI-7574c	216	A G ---	---	GCACAGCAGAATGAGCGGTGTGAGGAAGGTCCCTTTTCCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAAATGAGTTGGACAGTTCTTG ATAGCCAGGGC[A/G]TCTGCTGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAGAATGAGCGGTGTGAGGAAGGTCCCTTTTCCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAAATGAGTTGGACAGTTCTTG ATAGCCAGGGC[A/G]TCTGCTGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAGAATGAGCGGTGTGAGGAAGGTCCCTTTTCCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAAATGAGTTGGACAGTTCTTG ATAGCCAGGGC[A/G]TCTGCTGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAAAGGCGGTACTAGTTTCAGACACTTTTGGAAGTTTGTTG TCTGTTTGTAAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCCTTATCTACATTTACCTAC TTTGTAGTGAGAGACAAAGCAANNNNNNNNNNAAGAAAAATAAAC

WI-7576b	168	A T ---	---	AATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAACATAAGAGAGC CTTGTTTCATCAGTGTAAATAATTTTGAAGGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAA[A/T]GTTGAAGGCCCTTATTCTACATTTACCTAC TTTGTAAGTGAGAGAGACAAGAAGCAANNNNNNNNAAGAAAATAAAC
WI-7577q	77	T C ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCA[T/C]CAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	G C ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTT TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157	G A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAAGTTTCATTTTGGTTTACAC[G/A]TAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48	A G ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTT TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	G A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T C ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTT/C]ACTTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	C A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAAGTTTCATTTTGGTTT[C/A]ACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117	A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	77	T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577h	50	G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577g	157	G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAA AGAAGTTTCATTTTGGTTTACAC[G/A]TAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577f	48	A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577e	84	G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577d	93	T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATT[C/A]CTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577c	154	C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAA AGAAGTTTCATTTTGGTTT[C/A]ACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577b	117	A G ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAACATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	G A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAG[G/A]GTTTGTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAACATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619q	106	C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTC[G/T]CTGTGTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCT[C/G]CTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCT CGCTTTCTTCTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAA[C/T]GAGACTCTCTGTGTGGGGTGCTAATTACA TGGCAGGAAGAAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCAT[A/C]CTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCTCTCT CGC[T/G]TTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG ATGGCAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCC[T/C]CTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCTC TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACAT[A/G]ACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACA TGGCAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCCTATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCAATGGGGTCAATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATATGTTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGC[A/G]TTAAACCAATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGTCTGTTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATATGTTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCAATCATGACCAAAATGTGCCA TACTAATGATGAGCAATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGTCTGTTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATATGTTTAAACAAACAAAGCAACAGTAA TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCAATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGTCTGTTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626	144 T C ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATATGTTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCAATCATGACCAAAATGTGCCA TACTAATGA[T/C]GAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGTCTGTTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	---	TCCATAACCGCTGATTCAGGGTCTCTGTGCTGCCGCCACCCAGATGGGGGAAAGCAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCCCTAA[A/ /G]TAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134 A G ---	---	---	TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATTTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ---	---	---	TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATTTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ---	---	---	TGGAGAACATTCAATCTTGCCGTCACCTATTCATCAATGAAGATTAGAJCACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTACACGATGGTAGTGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGGATGTTCCAGTGGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACCTATCAGCAGCAACAACCTGTCAGTTTCATCC
WI-7703b	164 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAATTCJGGTCTCTCAGTTGTTTATTTAACCTCTAAATCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAATTCJGGTCTCTCAGTTGTTTATTTAACCTCTAAATCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---	---	---	TAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGAC[C/A]CCAGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAAACAGCGCTCCTGTCTGCCAGCCAGCAGCTCTCAGCC
WI-7743d	275 C T ---	---	---	TAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGAC[C/A]CCAGAGTCCCTGGTAATAAGTACT TACAGAAATTCGTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAAACAGCGCTCCTGTCTGCCAGCCAGCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---	---	---	TAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGAC[C/A]CCAGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GAGGGCAGAAACAGCGCTCCTGTCTGCCAGCCAGCAGCTCTCAGCC

WI-7743d	275	C T ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAG/ATTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106	C A ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C T ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743c	106	C A ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275	C T ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	106	C A ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275	C T ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7758	144	A G ---	---	TGACATTTATTCAAAGTTAAAGCAAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAAA GATAAATGTGTAATTTTGTATTATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C	---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCCACTGCCCTTTGACCTGCCCTCCCTTCATGCATGGAAATCCCT TCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[C/C]TTAGG GAAACATTCATCCTTGAGTCAAAAATCTCAATCTTCCCTATCTTTGCCACCCTCATGCTGTGTG ACTCAAACCAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTGCGA
WI-7773b	237	C G	---	---	TTAATTTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTTATCCGTAGTTTT GATAAAGATTTTCTATTCTTGGTTCTGTGAGAACCTAATAAGTCTACTTTGCCATTAAGGCA GACTAGGGTTCATGCTTTTACCCTTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C	---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCACCTCCAGTAGCGAGAGCGGCCACCCAGAAT CAGATCCAGCTTCGGCAATTTGATCAGACCAACAGTGTCTTCCCGGGGAGGAAACACTTTTTTAA TTACCCTTTTGCAGGCACCACTTTAATCTGTTT[C/J]ATACCTTGCTTATTAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTGTCCATTGATGATGATTTATTTGTAAATGTATCTTGGTGTCTGC
WI-7785b	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTGTCCATTGATGATGATTTATTTGTAAATGTATCTTGGTGTCTGC
WI-7785	156	T	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNI- JNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCATAATTTATTTGTCCATTGA TGATTTATTGTAAATGTATCTTGGTG
WI-7789c	84	G A	---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	G A	---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ---	---	TCTCCCCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACCTTTCACAAACCTTACAGTCCCTCCTAAGGTTACTCTTCATGAGATTATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTTCTTGAACCTC[G/T]TCTATACCTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTTAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACCTTTCACAAACCTTACAGTCCCTCCTAAGGTTACTCTTCATGAGATTATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTTCTTGAACCTC[G/T]TCTATACCTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTTAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACACATATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACACATATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAAATTTGACTTGTATATTTAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAAATTTGACTTGTATATTTAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAAATTTGACTTGTATATTTAAGAAATAACAGAA

WI-7830d	150 C T ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGTTC/TJTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTTTGTGCTGCACCTTTTACTTTTTTGGGTGTGGA
WI-7830c	54 G A ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAAGTCTGTCTGTCTGATGA TGATGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTTTGTGCTGCACCTTTTACTTTTTTGGGTGTGGA
WI-7830b	134 G A ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTTTGTGCTGCACCTTTTACTTTTTTGGGTGTGGA
WI-7830	44 A G ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAAGTCTGTCTGTCTGATGA TGATGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTTTGTGCTGCACCTTTTACTTTTTTGGGTGTGGA
WI-7865e	25 C T ---				CCACTTCCTATCTGATTTTCCAGG/CJ/AAATGAGGCGAGGCAATTTCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191 C T ---				CCACTTCCTATCTGATTTTCCAGG/CJ/AAATGAGGCGAGGCAATTTCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25 C T ---				CCACTTCCTATCTGATTTTCCAGGCAATGAGGCGAGGCAATTTCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191 C T ---				CCACTTCCTATCTGATTTTCCAGGCAATGAGGCGAGGCAATTTCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCAGGCAATTCCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGAATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCAGCAAAATGAGGCAGGCAATTCCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAGAATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCAGTCCCC CTAACAAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCAATTCCTGTTCTTGTCTATAAATCTATGT CTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCAGTCCCC CTAACAAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCAATTCCTGTTCTTGTCTATAAATCTATGT CTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGCTTT CACCCAACCTGCTCCCTGATCCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACACAAT CATTTAATAATTTCCCTGTCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGTCCTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGCTTT CACCCAACCTGCTCCCTGATCCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACACAAT CATTTAATAATTTCCCTGTCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGTCCTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66 T C ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGCTTT /C/TCCACCAACCTGCTCCCTGATCCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACAC AATCATTTAATAATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGTCCTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGGGGAATCC[T/C]ATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGA GCTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATCTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCAGCTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCAGTACAGTAAATTTAAACATCATTAATGCCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATAATCAATTTG
WI-7889c	54 C ---			TTAGGTCATGCCCACTCCCCAGGAGCAGCTGGCAGCTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAGTCACCTACAGGACTGGGCCGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCAAGGCTGTCTCTCCAGAGCACAAAGAAG
WI-7889b	54 C ---			TTAGGTCATGCCCACTCCCCAGGAGCAGCTGGCAGCTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAGTCACCTACAGGACTGGGCCGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCTCCAAGGCTGTCTCTCCAGAGCACAAAGAAG
WI-7894c	142 A G ---			AGCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTAATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATTCCTATA
WI-7894b	142 A G ---			AGCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTAATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATTCCTATA
WI-7900e	84 C T ---			GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33	C T	---			AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTTGGTTGGGTCGCTGGTTATTGGGCGAGCGCCGCTGGTCTGT CACACAGTCGCTGTGCATGCTCTGTGCATACAGACAGGTAACTAGTTCT
WI-7901b	33	C T	---			AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTTGGTTGGGTCGCTGGTTATTGGGCGAGCGCCGCTGGTCTGT CACACAGTCGCTGTGCATGCTCTGTGCATACAGACAGGTAACTAGTTCT

WI-7901	33 C T ---			AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGTAAGAC CCTTTTAAACAAACTCCAGGCCCTTGTTGGGTCGCTGGTTATTGGGCGAGCGCGGTGTCGT CACTCAGTCGCTCGCATGCTCTCTGTATACAGACAGGTAACTAGTTCT
WI-7901	271 T G ---			AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGTAAGACCCT TTTAAACAAACTCCAGGCCCTTGTTGGGTCGCTGGTTATTGGGCGAGCGCGGTGTCGTAC TCAGTCGCTCGCATGCTCTCTGTATACAGACAGGTAACTAGTTCTGTGT
WI-7926c	150 C A ---			CATTCGGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACACAGTGATTTGGGAATGCCCTTCATT TACAAATGCAATACTTA[C/A]ATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATAATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7926b	28 A T ---			CATTCGGCATCTGTCAACCAGGACAGAAATGTCATGGACAAGGGATGAGCTTTACAAAGATGATGCG ACTTTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACTTACATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATAATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7926	150 C A ---			CATTCGGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAGTGATACAAACACACAGTGATTTGGGAATGCCCTTCATT TACAAATGCAATACTTA[C/A]ATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATAATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7947b	203 G T ---			AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAATCCATAGATTTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCGAGTGCTGCCACCTG
WI-7947	203 G T ---			AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCCAGCCGAGGCCACAGAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAATCCATAGATTTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCGAGTGCTGCCACCTG
WI-7963b	145 T C ---			CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAAATGCC ACAAATTTTCATTTCTCCTTCTAAGTATTACAATGGAGTTTATTCTCTGCCTAAAGTGGAAGAAAT TGAGTGAATGA[T/C]AATTTTGTAAATTTAGGATAAGATCCAAAGTTATTTTCCCCAACTCTTGTTTCCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTATTAAGGCAGGAAGACGGGAAA

WI-8021b	57	C T ---	---	---	ACAATCTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATTCATCTGGAAC[C/T]GATCCC ACGTCCTTAGAACCTTACCACAAAGGAGTTTCTTGTAGTATTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCCCTTACATTTGAGATTTCTTTTGGCCCTCTTATCAAGTCAGCACACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTTAGGGTGATTGGAATTCGGTGAATTGCCA
WI-8021	57	C T ---	---	---	ACAATCTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATTCATCTGGAAC[C/T]GATCCC ACGTCCTTAGAACCTTACCACAAAGGAGTTTCTTGTAGTATTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCCCTTACATTTGAGATTTCTTTTGGCCCTCTTATCAAGTCAGCACACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTTAGGGTGATTGGAATTCGGTGAATTGCCA
WI-8024c	206	A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCATCAACAACCAATTTAGCCGCTCTAGCCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8024b	206	A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCATCAACAACCAATTTAGCCGCTCTAGCCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8077	167	A G ---	---	---	GAATGAGCCTTCTAGCGCCGAGGACCTGCTGCTGTTGTTGGCCTGCACATGTCATCTATGGAATGC TTTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNNATCTGCCAAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAAACC[A/G]TAAATTCATCAGATGGATTTTATTAAACGTT GTGTATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAGAA
WI-8118f	114	G C ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGC TATGTACTTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGA[C/T]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAATACAGAAATGTAGCTTGTTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC[T/C]GGCAATACAGAAATGTAGCTTGTTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCCTCGGGAAG AGGGGTAGGAGACCAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAACI[A/G]TGGCAGCGGCCTCGGG AAGAGGGGTAGGAGACCAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAACI[A/G]TGGCAGCGGCCTCGGG AAGAGGGGTAGGAGACCAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCCTTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCCTCGGGAAG AGGGGTAGGAGACCAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACGTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGTAACCACT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCT[G/C]TAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACGTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGTAACCACT

WI-8321	178	G A ---			TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---			TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---			TATGTACTCACTTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCAGCCTTAGA[VC]ACTAAGTAG CAGTACTGTTGGTGTGTGTTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---			TATGTACTCACTTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGC[VC]AGCCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTGTTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---			TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAAGAGAAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCCTCCAACACGTGGGG
WI-8378	308	T C ---			TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAAGAGAAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCCTCCAACACGTGGGG
WI-8426	184	T G ---			TTAGCACATATTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTAACACAG TTGTTGTAGACTGTTAANNNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTTCTTTTGTCTGGANGGGTGGCTTTTGTCTTGAACCTTCCATTCTGTTG/GCCTTGTAGCTGGTG AGGCTGGAGTATGGANGGNCCTGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A ---			TTGAGCCTCCACAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTGAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAAATGCAATTCAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTA[T/C]TTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTA[T/C]TTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTA[T/C]TTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAAGTTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTACAAAAATACGTTATTTTAA[A/G]CTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTACATTGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105	A T ---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461b	38	T C ---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461	38	T C ---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461	105	A T ---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTGCAAAAAGGGGG
WI-9438	77	A G ---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGTAGTACCTTAATTTTGTATAAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAAAATTAGATTATGTACAAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATTTCTCCCTTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101	C T ---	---	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCCTGTTAACCTTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGACACACTGTACCATCTCAGTCCCCTCT GCCTGTAACCTTAGAAAAACAGCCCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGACCTGTAAACAAAAG
WI-9439a	76	C T ---	---	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCCTGTTAACCTTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT[C/T]CCAGTCTGTCAGCTCAGTACCTGTCTGTGACACACTGTACCATCTCAGTCCCCTCT GCCTGTAACCTTAGAAAAACAGCCCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGACCTGTAAACAAAAG
WI-9446b	75	T C ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCCAAATGACCANGNCATAAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTGNCCTACTNTTATCACTGTGCTCTTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75	T C ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTACCATTCATAGACTATAAAGANCATTA TAAAAAAAT/CJCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTGNCCTACTACTATCATCTGTCTCTCTGCTCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A --- ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCAGGCTTTCTCTAGATGTAAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTTNCCTTAAATCAAGTATGTAAATGTCACTT GGAATTCATACATGGAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9497	185	A --- ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCAGGCTTTCTCTAGATGTAAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTTNCCTTAAATCAAGTATGTAAATGTCACTT GGAATTCATACATGGAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9523b	193	C A ---	---	GTGAAAAAGTTTTCTATTTCATTCATCATACATAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTGAGAAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTTCAGCCATGATCTATGGTGATTTTCCACACATTGTAT[C/A]JAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9523a	47	G A ---	---	GTGAAAAAGTTTTCTATTTCATTCATCATACATAATAGATTGTGCTAAG[G/A]JATCATTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTTCAGCCATGATCTATGGTGATTTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9554	202	T C ---	---	AAAAACACAAGTTTCATACATACACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGTACTGCTTTCCTTNCCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GTT/CJGCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---	CCAAAGCCCAACCATTCATATGTATGGATTTCATAAACCATTTATTGATCCTTTTTTGAGGTAAGTAT AAATACCTTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCACAAATGATCATACTTTCAGATTAAATACAGGTAAGTATTTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCCTTCACATTGATCACA
WI-9625b	172	A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATCTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTTACCATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATCTTGGAAAAAAACACGCACA TAAGTATCATAAAGTGGGTTGTGGACAAGTTACTTCTTA/TGGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTTCATCCTTTCA ACATCTTTTGTACACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACT[C/T]GTCCCTTTACCTGATACATTTATCCATTTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGICCCCTGCTTTTGTAGTTAATTGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGAGG[C C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGT[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT[C/CCCTCTGTGCGCATGAATAAATTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT

WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCG[GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT/C]CCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC[CCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC[CCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT
WI-9676a	84	A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTG[CCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGT

WI-9738b	40 C A ---			TGGACCAACACAGACAGATGTATTCCTGGTGCCTGTGTATC/AJATTACAACCTCATTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTGTGCACCTGCTGGAGCGGGGTGTTTTCACTATGTGAGTATCTA TCITTTTATTCTGTCCCTTATGTTGGTGGCACAATGCTGTATTGCTGTCC
WI-9738	40 C A ---			TGGACCAACACAGACAGATGTATTCCTGGTGCCTGTGTATC/AJATTACAACCTCATTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTGTGCACCTGCTGGAGCGGGGTGTTTTCACTATGTGAGTATCTA TCITTTTATTCTGTCCCTTATGTTGGTGGCACAATGCTGTATTGCTGTCC
WI-9756	47 A -- ---			ACTGAAATGTAAATGGCCAAAGGCACCCAGGACCCTTAAAAATCATAAGAAAGTTAATCTGTGGGAAAA GAGTAACACTACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAAATGTGTCCCTTATCAGCTTTAGTC AGTAAAGATAAGAAAGCCCTGTGTGAGTATCCACTTCCACAAACACACAGATATACACTTTTGGAAAG ATTTCCACTTAACCACTTGATTCTTCACTTTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135 A G ---			GATGGTCCCTTAAGGATTGTCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAAATTCAAATTCAAAGAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/A/GJTAAATAACTCTGTGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAAACCGCTGGTTCTAAAT ATTACG
WI-9778	127 G A ---			ATTTAAATCCAGGCGGGGAAAATGGATACCTTTTCATATGTCTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTTCATTTTGCCCTTCTCACTCCAAAGTACCAGTATTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCTCTCA AAGATGTGTGCTCAGTCAAGGAAAGGCAATAGTCTCAGGCAGACAGCC
WI-9832	116 C A ---			TCCTCCCTTTGCCCTCTCATGCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTTCTC/AJTGATCCACCCAGGA CTCAAAAAGACTAGGAATTTGGGAGAGAGGACCTGGAAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCCAGACATGGAAGGTGGCTTTGGC
WI-9841	101 A G ---			TGGAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCCTCATTTTGAATGAATAAAATATAC/A/GJTGATGTATATATATACTTATTAAACACTT AGGATTATATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTGTTACTTGTATGATGCTGTTG
WI-9880c	222 G A ---			GAACTAACACCTTTCTTGATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTGTGTGGGTTGAGTTTTTATGATATCTCCTGTAGACCCCAATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACATGAA AATGGAATGAAATAATGA/GA/JTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---				GAACTAACACCTTCTTGCGATTTTCTTGATTATTGGCAGTTAACATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGTTGAGTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C/A]TATAAGATCCTCTTTTAAATTTATATTTTATATAAGCACAT GAAATGGAAATGAAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---				GAACTAACACCTTCTTGCGATTTTCTTGATTATTGGCAGTTAACATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGTTGAGTTTATGATATCT[C/T]CTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGAGCTATATAAGATCCTCTTTTAAATTTATATTTTATATAAGCACAT GAAATGGAAATGAAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---				ACACTGCAGGCACTCCAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAAACACGCCCCAGTTATCACAGTTTCTNTTTTTGT[C/T]CACCC ATTTCCATAACAAAAGAGCTACACAAAATTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCAATGAATAATGATTCCAAA
FB25G10b	109	A G ---				TCCCTCAATGACAGATGAACATAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACGTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---				TCCCTCAATGACAGATGAACATAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACGTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A ---				ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTTCTTAAACCCTAATGAGATTTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAAATATGACCCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---				CGTCCTTTCCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTTGTCOC TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCCCAATCCACCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTC
S72904	51	G T ---				AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTTCCTTT[G/T]AATTTGTCAGTTC ATTCTGGAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCACAAAGTGCTGTAACTTCTCCCTTCTGTCAATTGGTTGCTTTAAATA TTGCAAAAGTCTGTATGCTAAACAGTATTTGGAGTGTTTCAGTGCTGTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAACACAGAG[C/T]ACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGACAAAAATAACNAGAGGCATCCACGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGACAGTGACC
ESTC110	23	---	---	---	AACTCCTCACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAGTTCCTATCACAAATTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCCTTT
ESTC122	34	---	---	---	GACAAATAACACAGCTAAGCTACTGACATAAAATATNCAATAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCGCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGAACTGG
ESTC129	20	---	---	---	AGTCACCATGCCCGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGCTGTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAAGGTAGACAAAAACATAAATCTTCAGGAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCCTCANAGTCTCTCCTCAIGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCCATTTCCTAACAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATAATTTCTTGACATGAGGTNGCTTTTTAGCAGCATTTCCGG
ESTC146	20	---	---	---	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCTTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGCCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGTCCTGAG
ESTC149	28	---	---	---	TCAGTTCATTTATTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAACAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCAATTTTCTTTTCTTTTAAATACAAATCTACTGTGCTNAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	---	---	---	GCAGCATTTGTACAGGAGAGGCGCAACAANCCTGGCTGCCCTCGGATGGAGCGGGCGGCCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTTGCTGTGCAAGTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCAGTGGGCCGCTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTTGCAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAAATATTGGTTTGTAAACANCGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCCTGTGTGTCAGGGAATCANTTTGCTGGATTAGAGGAAAGTGCCGCCGCTCTGTTCATGACTT
ESTC176	23	---	---	---	---	CACCTCCTCCCCTGAGCTACCCANGTAGTGTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCITTTATTTCTATTTAAATACCTTTTAT TCTCTTTATTCCTATAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCTGTCAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATAATAACATATTACACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTACACACCNCTGTCAACCTCAAAACAGATGATACTCATCCTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTCCCTAACTTATCAGTCTAGTAAGCNTTTCAAGGAGGAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCNGCAAAGTCTCCCACAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACCTCCAAGAATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAATCCCAATATATGAGTTTAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCTGCAACAG

ESTC201	35	---	---	---	TCTTACTTGGGTAGTTTAGCAACATTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACGGNCAGCGGCTGGGTGGCGCCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAATAATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGCTCTCAGAGCAGAGGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCCTCCANACCAGGGGCGAGGGAGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAATAACATTAACAAGTTCAT AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAATTTATGGGTTTATTCTTATTCTAATTGNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCCAAGAGAGGGGCGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	TTCTACTTTATTTCATATTCCACCACNATAACGACTCCTTTAATTTAAACTAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	GCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTAGTCATATTCCCCANCAACAGCATGATAAAATAATTC AAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTTCTCCTCTATTCTCTATAAAATAAAGGAAGCAGAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTATTTCTTGAGCCGCTTGGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATATNTCAGTCGGTGATCATTGTAAATATACAATAACAAAGCAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAAC TTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAAACNCTCTCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGGCCAGGAGCCACTGGTGCGGANCCGGCAGATGTTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCCAAGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTNGTTCAGACTTCAGGAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAAAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGGTTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCCACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCCCACGGGAGGTGCGGGAGACGACACTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTAAATCCCCACACTTACTTACTGCTCATCCGTCACCTTCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGCGGCCAGATAGCTGTCTGAGTTGCANGCACGATGGAGATTGGACACTG

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNITTTGGCGTGACGCCTAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAATCAAAATATTCACNITGGGTTGAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTCCTGTCCCATCGGAACCCAGAGATTTCCTCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCAATGTCCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGINTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC83	53	---	---	---	ATTGCAAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAAATGA
ESTC85	28	---	---	---	CTGGTTCCTTCGTCCTGGCAATTCGTCCTCCTCNGGCCAGTGTCTCCACCCCAAGTGTCTCCCGATGAT
ESTC89	22	---	---	---	CTCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTCAAGGCAGGATCC
ESTC90	33	---	---	---	GCAGTTCCTTTGTTCTCCTCTCCAGAAAGTTGNAGACGTCATTTAGTTTGATTAICTGTGCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAAATTC GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGACTGTTCTCCA[C/T]GCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAAATCAAAGAAAGAAAGGCTTAGCTG
DWU-100	127	CT	---	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGTGAA TGTTCAATGGC[A/G]GCCCTATTCACAGTAGCCAAACGATGAAACACACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAAAATGTGGTCCATCCATACAAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	A G	---	---	CAATACCTGGACTATCAACCTTGTTCCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCCAATCATGCCAGCTTCTGTCAATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAAACCCAGCCCTATCTGAGTCTTCGGCTCCCTCC
DWU-286	213	A C	---	---	

DWU-252	94 A G ---	---	AGTATACAACAATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCCCTCA[AG]TGAGCATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCAATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCCTGTTGAATGACAAAGTATGTGTTTGTGTA AT
DWU-330	85 C T ---	---	GAACATTCCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCATTATGTGGACTGAA[C/T]CGACTTTTCTAAGCTCTGAACAAAAGCTTTTCTTCTTCTTCTGCAA CAAGACAAAAGCAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAATGTTAATTGGGCAGGTGAAAAGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCTT[AG]GCATCTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACCTTCAGTCCCTCATCTATAAGAATAAGGGATTTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC[AG]TGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACCTTCAGTCCCTCATCTATAAGAATAAGGGATTTCAGTTGTGATCA[C/T]ATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTTCCCTGTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG[C/G]AGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTCCTC
ESTD-ADAa	184 G A ---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTTCCCTGTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTC[G/A]GCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTCCTC
ESTD-ANT1	160 T C ---	---	TCTCCTGTCTACTCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGAAGTCCCAACTGCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
EST10398	168 A G ---	---	TGCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGCCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTGATGTTGAGGCTTGACTTCCAAACACGGAGAAG CATTGTTTCTTCGGGCCCAAGAAAGGTATCTACC[AG]ATAGTGTCTATTAGGCATTTG

EST10398 2a	147	C T	---			TGCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTATGATGATGTTACATTTGGGGCTTGACTTTCCAAACGGAGAAG CATTGTTTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGCTATTAGGCATTTG
ESTD-C7	14	G C	---			ATAATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90	T C	---			CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTTCTTTT/CCTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38	G A	---			AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTTCAACC/GA/CCGAGAACTGCTCGATATC
ESTD- HRASb	82	A G	---			CTGGGCTCGCCCGCAGCAGCTGCTGGCACTGGACGGCGGCGCCAGGCTCACCTCTATAGTGGGTG TATTCGTCCACAA/A/GTGCATCTGGATCAGCT
ESTD- HRASa	37	C T	---			CTGGGCTCGCCCGCAGCAGCTGCTGGCACCTGGACGG/C/TGGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81	A G	---			GGAGCAGGAGGTGGGAGGGGTCTGCTGCTCCAGGTCCACAGACCAGAGAAGCGGCTCAGTG TATCCCCACCCCCA/A/GTGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A G	---			GTGACCTTCTCACITTA/A/G/AAACTTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAAACAGAAAGGAGAGGTATGTAAACA
EST36751 7	36	C T	---			CCAAGTCGTTCAATTTTAGCTTTCAGGTTTAACT/C/TGATTACTTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109	A G	---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACTGGATGCATTAAACAAAT/A/GTTTTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCTGACGTTTTTGAAACAATACA GATGCTTCCCTGTAGCAGTTTTCAGCCTCCTCTACCTA
EST18288 3	121	C T	---			GCTCTATACCCCTGTGGTCCCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCCCTGA/C/TGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31	C T	---			GGGAGTGACAGCTAGAGCACCAAGGGGGCT/C/TACAGCTGTGTTCTCATGGAGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180	A G	---			AATCCCAGCACITTAGGAGGCTGAGGCAGGCATATCACCAAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAAACATGTTGAACCCCATCTCTACTATAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCG/A/GJAGGTTGTGGTGAGCCCGA GATGGCACCATTTGCACTCCAGCCTGGGCAACAAGAGTAAACTCTGTCTTC

EST70523 3	182 G T ---			TTCCCGCAGCCCCCATCCTTGGCACCCCTGGTCCCTCAGGGCCACCCCGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCCGGCGGCTCCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGAGGCCCTTCTGTCCCGGCCCTTCCAGGGGCCAGCCCTTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGAGTGTCTCCACGTG
ESTD- APOA2	101 C T ---			CCAGGTGTTGTGGCAGTGCCTGTATCCAGCTACTCGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGTCCTGCCACTGCCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---			CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6	137 C ---			AGACCATGAAGGAGTTGAAGCCCTACAAATCGGAAGCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGAGCTGCAGGCGGCGCAGCCCGGCTGGCGCGGACATGGAGGA CGTGGCGGGCGCCCTGGTGCAGTACCGGCGGAGGTGAGGCCATGCTCGGCCAGAGCACCCGAGGAGC TGCGGGTGGCCTCGCCTCCACCTCGCGCAAGCTGGTAAGCGGCTCCTC
EST43211 8	132 C ---			CGCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCC TGCCAGTGTACAGCGCCGGGCGGCGGAGGGCGCGGAGCGGCCCTCAGCGCCATCCGCGAGCGCCTG GGGCCCTGGTGGAAACAGGGCGCGTGGGGCGCCACTGTGGGCTC
ESTD- ARSB	126 A ---			GGAAGAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGCGGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCCATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAATTTGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACCTGCATCATTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCCCTCCCGATAGGGCTGGGCTGACCCAAATAATACTGGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTTACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGAGTTGAGTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCATTCTACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGCAACAAGACAAAGCAAGCC
ESTD- BA511	29 A G ---			GGGCAACATAGTGAACCCCATCTCTACA[N/G]JAAATAACAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTGCCACTGCA

ESTD- CB22	119 C T ---			G G C A A G T T T T T A T T G A T A G A G A G A A A T C A A A T A A T G G C A A T A G G A G A C A T C A C C T G G A A T G T T A G G C A G T G C C T A A C T G G G G A T G G A C A G A C A A T G G C A G T G C C A A C C C A T A G G G [C] T J G G A T A C A A A A G A C A G G C A A G G A A G G G T A G A A C C A T C A A A G A G A A T A G G C T G G T G A C C C C A A A G C A A G G A G G A C C T A G T A C A T A A T T G I C T T C A T T A T G G T C C T T C C G G C C T T C T C T C T C A C A C A C
ESTD- CB23	136 C ---			T A G A A C C A T C A A A G A G A A T A G G C T G G T G A C C C C A A A G C A A G G A G G A C C T A G T A A C A T A A T T G T G C T T C A T T A T G G T C C T T T C C G G C C T T C T C T C A C A C A T A C A C A G A G C C C C T A C C A G G A C C A G A C A G C T C T C A G A G C A A C C C T A G C C C A T T A C C T C T C C C T T C C A G A G A C C T G A A A A C G T G T T C C C A C C C G A G G T C G T G T T G A G C C A T C A G A A G C A G A T C T C C A C A C C C A A A A
ESTD- CB24	145 A ---			A C C A G G A C C A G A C G T C T C A G A G C A A C C T A G C C C A T T A C C T C T T C C C T T C C A G A G A C C T G A A A A A C G T G T T C C A C C C A G G T C G T G T T G A G C C A T C A G A A G C A G A T C T C C A C A C C C A A A A G G C C A C A C T G G T A T G C T G G C C A C A G G C T T C T A C C C G A C C A C G T G A G C T G G T G G T G A A T G G G A A G G A G G T G C A G A T G G G T C A G C A C A G A C C C G A C C C C T C A A G G A G
ESTD- CB25	146 A G ---			G T T T C T T C A G A C T G G C T T A C C T C C G G T A A G T A G T C T C C T T T T T C T C T A T C T T T C G C C G T C T C T G C T C T C G A A C C A G G C A T G G A G A T C C A G G A C A C A G G G C G T G A G G G C C A G A G C C A C C T G T G C A C A G G T A G J C C T A C A T G C T C T G T T C T T G T C A C A G A G T C T T A C C A G A A G G G T C C T G T C T G C C A C C A T C C T C T A T G A T C T T G T A G G A A G G C A C C T T G T A T G C C G T G
ESTD- CB27	125 C T ---			T T T T C T G T T C C C T G A A G A T T G A G C T C C A A C C C C A A G T A C G A A A T A G G T A A A C C A A T A A A A A A T T G T G T T G G G C C T G T T G C A T T C A G G A G T G T C T G T G A G T T C G T C A T C A C T G A C [C] T J A T C T T C T G A T T A G G G A A G C A G C A T C C C T T G G A C A T C T G A A G T G A C A G C C C T C T T T C T C T C C A C C C A A T G C T G C T T T C T C T G T T C A T C T G A T G G A A G T C C T C A A A C A C C A T T T C C A T A C C
ESTD- D4S338	59 A T ---			T T T T C T G T T A C C T T G T T C A G A T C C T T C A G A G A A T C C C T A T A T A T G G C A G G T A T A T A T A T A T A T A T A T T T C T T A A C A A T A A A C T T G A A A G T C C A A A T T A C T C C T T G A T C C A T G G A C T G C A G A A T A A A T G T T A T T T T A G C T G T C A G A A A A C A A T A C T A A T C T T G C A T A T G T T C A T C A G A G C C C T T G G G T G A C C A G G T G T A T T G C C A A T A A G C A G T A A T A T T T G A G A G G A T C T T G T T T C A A T G C A G T A G
ESTD- CYP2D6	61 A G ---			C A G G C C A G C G T G T C G A G G T G G T C A C C A T C C C G G C A G A G A A C A G G T C A G C C A C C A T A T G C [A] G J C A G G T T C T A T C A T T G A A G C T G C T C T C A G G G T T C C C C T T G G C C T G A G C A G G G C C G A G A G A C A T A C T C G G
ESTD- D11S1873	40 A C ---			A A A A A C A T T T T A A C A C C T T T T C A A T C A T A T A C A C C A T A [A/C] A T T T C C A T T T T C A C A T A A G T C A G T T T G A G C T G A G T T T C C A A T T A C T T G C A A T C T A A A T G T C A T A A C T G A T T A A T G C A A G T T C A A C A G A C A A C T T T C C C A A G C A T C T A C G A T C A G A A A G T C A A A A T A T T A C A T A T C T G G A T T A A A T T A T G C C C A T A T C T G C A T G T C
ESTD- D17S33b	169 C T ---			C A T C C C A A G C C C A T C C T T A G C C A C T G G C A T T T T T G C C G C C T C T G A C A G A T A C A C T A G G C C G T C A T G C T G C A C A C A T C C A G G G G C C C C T A C C C T T T G T A G T C C A T G G A A A G G C T C C T C T G G G G C G G T G G G G T T G T G G C T A T G T G G T C T T G T G T A G A [C] T J G G G G C C T T T G G T T C A G T T G C A C T A T T G C G T T A T T G C A G A T T G C T T T G C T T T C C A C C T G A G C G A G C C T C

ESTD-D17S33a	75 C T ---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCAATTTTGCCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTG[C/T]ACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGTGGCTATGTGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD-D18S8	133 A G ---	---	TTTGAGACCACCCCTGGCCACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCCTATCGTATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATTGCTTGAACCC[A /G]GGAGGCAGAGCTTGCAGTGAGCCAGATCACACCACCTGCACCTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD-D3S11	44 G -- ---	---	AACTGATTAGAACCTGAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCATTTGG AATTTTGCATCATTAATAAATCCCAATAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACTTATTTTATTTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGTGCTGATGTTTC[C/G]GGAGCCCTTGATGTCATTTCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTTAAATTCAAAGGT TGAACATAAAGTA
ESTD-D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTTCCC AGAAGTGAAACATACTGCTCCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTTGGAAGGATGC[C/T]GGT
ESTD-D3S2a	248 G -- ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTTCCC AGAAGTGAAACATACTGCTCCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTCTACAAATGTATAATCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCC[C/G]GTCTCTACATCATCTTTTCAACAAACATTTTCATCCATGGACTCCATAC TAGAATATTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGCGCTTGACCGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGAGGTGGGAGGGAGACA GAACTGCTGATT[C/T]CTGGTGAGAACCAACCAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGCGCTTGACCGTGTGGCTCAAGCAGCTGCTCGGCCTCC[C/ G]TTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGTGGGAGGGGAGA CAGAACTGCTGATTATCTGGTGAGAACCAACCAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGGAAGAGAACAGAGT

ESTD- DRD1	154	C T ---			TCCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCATCAC ACAAACGGTACAGACCCAACTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGG[C/T]TCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144	C ---			TCTGCCCTTTGGTGCAGGAGCTGCCCGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGAACCCGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCGCCAAACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109	C T ---			AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTACAGTGGC[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCACAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD- ERBB2	93	C T ---			TCTTTCAGGATCOGCATCTGCCCTGTTGGGCATCGCTCCGCTAGGTGTACGGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGTC[C/T]GGGGGGCGGTGCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACCTCGTTTCTCGACAGCTCCGCTCGCATCGTGACT
ESTD- ETS2	43	A G ---			ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGACCC[A/G]GGAAGCCGCTCCTGGCGCTG GCAGTCCGTGGGACGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACA CACAGACTATTTTAGATTTCTTTTGGCTTTTGCACCCAGGACAGCAATGCAAAACTCTTTGAG AGGGTAGGAGGGTGGGAAGGAAACAACCATGTCTTTTTCAGAACTTAGTTTG
ESTD-F9	111	A G ---			AGATCCTGATGATTTTTTCTCTATTTTTCTAAATGTTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTT[A/G]GTCAAACCTTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144	A ---			CTTCCATGCGGATTTGACTTTATTTCTCCATTTGCTTACCTTTTACAGGTGTTAATATAGTGAAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAATTACACAAGAAAGGAATAAATTCACAGTCAA AGAATCAAGCACCTTTTCGAAACATTGAAGTTGTTTTTGAACCTTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GCDH	200	C G ---			CGCAGACCGGTGAGTGGGTCGGGAGTGTGGAGGGAAGGAGGGAAGGAGGAGGAGGAGGAGGAGGAGT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGGACCTCTGGTCGCACCGTGTGTTCTGTGCTGCCCTGTTTTCAGCTGTCTGTCTGCCGAGT[C/
ESTD-GCK	88	A G ---			GIGACTCTGTCGGAAATTCGAGAGCT GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA[A/G]CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCGAGCGGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62	A T ---			GTGGGGCAACAGTGGGAGAGAAGGGCCAGGGTATAAAGGGGCCCAAGAGACCGGCTC[AT] AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56	A G ---			GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCAC[A/G]GGCATCA TTGAAACCAAGTTTCCGTCAAGACTTGAATTCAGGTAAGTGCAATGGTTCCCTAGG
ESTD-HT2	154	G -- ---			GGGCTAAATTTCCGAGCACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTTACAGTTTGTACAGAGAGAATAAAAGGATAACCTGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149	C -- ---			AACACACAAGCCCCCAGCGAGAATTGAACCTCGCGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTCTTCTTCTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGTTCT
EST37382 5	124	A G ---			CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACAGCAAGAGAAAGAAAGG[A/G]CCCCAGA AATCACAGGTGGGCACGTGCGGTCTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGC[C/T]CTGGGAGAAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120	C -- ---			TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCCTACATTGTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAACCCA
ESTD-IL1A	110	A G ---			CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATATTATTATTATTTATTTTATTTT AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGAGTGCG[A/G]CAATCTCGGCTCACTGCAAGCT CTGCTCCTGGGTTTCATGCCATTCTCCTGCCCTCAGCTCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTACCCGT
ESTD-IL1B	99	A G ---			CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
EST74082	134	A T ---			TCCAGGGTGGCTGGACCCAGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGCGGGTGAGCCAGGGGCCCAAGGCAGGGCACCTGGCCTTCAGCCTGCCTCAGCCCTGCCTGT[C/A] TJCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGGCCCTCTGCCCTGTGCGCTGTGGCTGTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGCG

EST45311	0	151	C T ---				GCCCTCCTCTCCAAATCTGTCCCTATAGTTTCCCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAAACA CATTTTCTGCAAAAT[C/T]ACCTCTTTCAATTAACAGCCCTTATTCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258	8	80	A G ---				TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCC[A/G]CCCTCAAAATGACAGCCATGGCCGGCGGTGCTTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216	3	26	A T ---				ATGCAGGATGAAGGTGGACAGGAGG[A/T]GAGGGCCAACTGTCTATCCAGGGCCTGCAGATGTCTG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782		149	G T ---				ATACTAGTACAAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTTCTCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTTTCCCTC[G/T]AAGTGCCAGTATCCAGAGATTTTGGTTTTTGAACCTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTTGGGTTTTTGGTGCATGCA
ESTD- KRT10b		183	C T ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG[C/T]TGCTTTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a		133	A G ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTA[A/ G]GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b		231	C T ---				ACCTCACCCCTCCCTTAGCCGTTAGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCATATCTCTCCGTCCTCAGGTTTACCA[C/T]GTCAACATTGACACA
ESTD- KRT8a		21	C T ---				ACCTCACCCCTCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCATATCTCTCCGTCCTCAGGTTTACCACTCAACATTGACACA
EST75099	6	82	C T ---				CAC TTGTGTCTAGATCTCTCAGTGGCGGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA[C/T]GGGGGCAACCGGAAGACCATCTTTGGAGGATGAAAAGAGGCTGGCCACC CCTTCTCCTTGGCCGCTTTGAGGTGTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGGCTCAGTTAATTTCAAATTTGTAACCGTAGCAAACTGCATTGGTATTTAGA AAATATAAAATTTCCAATATAGTGTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGAAACCJAGJGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTTCTCCCAATCTTGCGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGACCCAGGCTGTACCCCAATTAGGTGAACATGGCTTCGAG AGAGTTGJACJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ---	---	TACACACTTTCCTTACCCATTCACTGAAACGACTCJGJGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCTTAGGGGCACCTCACACTCCAGCTTCTTCAGCTCTGCCCTGTCTGCCTGCCTGCA AGGTTTTGCTTAATCTCAATTCAATGTCTCTTCATCTTTTAGCJGJAGCTGTGGGTTTTGTTGTG TTCTCTGTTTTGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAAGTTCACAACTTTATTAATAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCTCCCGAGCTCTGTCCTAGCJGJGAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAAGGTTTGCTTAAGTTGCTGATTACCJGJGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACJGJACCAGATCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107 A G ---	---	AACATGGACTTGTATATTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTJAGJGCCCAAAACGTCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATTC GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	45 A G ---	---	TGTCCCTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCJAGJGTACTGCAAGAGAACACA GACAT
ESTD-NRAS	202 C T ---	---	GTGTTTTCTTAATCTTTTCCAGGAACACAGTGACCATATTTCTTTTCTGCAGGCATATAGAAATTTGGT GGGTTTTCTTTTATGAGGGTGATATTGGATACCTTTTGTGTTGTGATTATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTTAGATGCTTATTAACTTGGCAATAGCATTGJ CJTJATCCCTGTGGTTTTTAATAAAAT
ESTD-PAI1	100 A G ---	---	GCCACCACCCACCCACAGCACACTCCAACTCAGCCAGACAAAGTTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGJAGJGTCAGCCGTGTATCATCGGAGCGGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120 A	---			CTCTTCAGGAACCAACAGTCTTCTTACCAACACAGACTTATTGCTGTCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACACTTCTGTTCTAGAACGTTTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCC
ESTD- Per/RDS	74 A	G ---			ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGA/A/G/GAGCGTGCCTGGAGACCTGGAAAGCCCT
EST68308	5	29 C T	---		GGAAAGAGATTTAAGAAGCTTGATTTGGGAC/C/TJAATTCGGTTCITTTGAGTGTGGAAGATTGTC TCTGCCCTGAGTTACAACAGAAATCCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTTA
EST54045	6	39 A G	---		GGAAATATTAAAAATATTTAAATACCTCCATTTTGCTT[A/G]TCCCTTTTAGTGAAGATGATACCTG AAAAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88 A	G ---			ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTA ATGCAGAAAGAGGGGAAAA/A/G/GAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAAICTT
ESTD-RDS	127 A	---			CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGGAGAAGAGCGTCCCGGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAAGCTGGCAAGGCAACCAGGTGAAGCCGAGGCGCAGACGCAGG CCAGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- s14544	94 G T	---			TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTAATAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTT[C/G/T]CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45 A C	---		ATCACAGGTCTCTGGTCTCTGGCCATCATTTTCTGGGAGAGATGG[A/C]TGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C T	---			AGGAGAAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT[C/T]GGCTCAG GATGCCGGGAAATGAC
EST76136	39 C T	---			TGAAGCTTCTGCCAGCTTGCAATTGTTTCTAGGAGAACC[C/T]GGGTACATACCTTTATCTATAGCCTT CCCCTAGGTCTT
ESTD- SPTB	176 C T	---			TGAAACACCCCTGTGGTCCGGAGCCAGGTGTGTCTCTCCCTGGGAGCCCTGAGGAGTTTGTGTCTGTG CAGTCCCCCGCGCCACCTGTGTGTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTGTGCAACA[C/T]CCTCTGTGAAGACCCCAACCCCTGC CTCCCCCAACCAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	125 A C ---	---	TGCGGCCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCGAAGAGAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC[A/C]CTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD-TYR	122 G T ---	---	TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGAATTTCTTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAA CATGGGTGTTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGGATGACA
ESTD- TYRP1	222 A C ---	---	AGTAGTGGATGAAGCTAACGAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	AGTAGTGGATGAAGCTAACGAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- VB12	148 C T ---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCACAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

ESTD- AT3aa	60 C T ---			AGACCTCAGTTTCCTCTTCTGTAAAGGGAAGTTTGTTCCTGGATCTCCATGGGCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACACAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
EST39852 8	106 C G ---			CGGTCTTCCTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTA[C/G]GTACAGAAAGGAGATGCATGAACA GCAGGAACACGCTGGAAAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---			ACCTGGTGTGCTGGTCTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGCCCGGTGG TCCTCCTGTGTGCTGGTAGTCTGGAGTCAACGGTGCTCTT[A/G]GTGAAGCTGGTCGTGATGGCA ACCTGGGAACGATGGTCCCCCAGGTGCGGATGGTCAACCCGGACACAAAGGAGAGCGCGGTACCC TGGCAATAT
EST36027 2	120 A C ---			AGTGACTTCCAAGGAATGGCTACCCAACCTTGCCTTCATGCGCCTGCTGGCCAACCTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCATTTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---			AGAAATGTATATAGTCCCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTTCCTGTCACTTTC[A/G]GGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGCTGGTCCCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---			TGAGAGAACACCTAGTCCCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA[C/T]TGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATTTTATTTGACCAAAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---			GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGCAGATGAAAAGCTACCATCACTTCCCTCATCATGAAAC TGGGAGGCCGGGCAT[A/G]GTGCTCATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGGCGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ---			CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAAAATATTTCTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGGTCAGAACTGTTCTGTCAACCATGGAGGATACTATACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G --- ---			ATGCTAAGGGGATCGGACATGAAAGGAGCCCTGTGAGCCGATTGTCTCTATCTCCAGGGCCCTGTCTC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCAGTGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTACATTTGGGATTGTTTCTTTTGGTGTGAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGGCTTTGGCTGGCTGTGGGATATTTGAAAGAGAT[C/T]TTTGCCAGTCCAATGTCTCTAGAGATTTCCCAATGTTTCTTTGTAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATTTGATTTGATTTCTGTA
ESTD-RYR1	109 A G ---	---	CTTCGTACGGGAGGTACGTCTCCGCCCTCTTTTCATGGACATATGGATGAGTGTCTGACCATTTTCCCCTGTGACAGTGTACACGAGCGAGACTTTGTCTACTATGAG[A/G]GGGGAGCTGTGTGCACTCATGCCCGCTCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACCTGGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTGCG[A/G]CGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCAGGCTGCAA
ESTD-F2	100 C ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCAACTGTGCATGCACGCTTAACCTCTGCACCAAATGGCTCCAAGGCCCGTAGGGAACTGGGGGATCTAGGGATGGGTGAGGAATGGCCCCAGCCAGTCCCGGCCGGTGCCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC
EST44438	62 C T ---	---	TGGATGAGGCAGCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA[C/T]GTCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGGTGGG
ESTD-PBDA	103 A G ---	---	CCTTCTCATGCCCAGATGGAAATCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAA[A/G]TCTCTACCCGCAGCTTGTCTCGCATACAGACGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
EST12839	122 A G ---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[A/G]TCAAGTCCAAGCCATTGGCTATCTCAACACTGGTGTGAGTGATTACTTIGAGTAAGGAAACTTGAATGTTATTCAAC
ESTD-CTLA-4	48 A G ---	---	TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATATGATACTTAGCTTAGATGGCTTGCCTTGGATTTCAGCGGCACAAAGGCTCAGCTGAACCTGGCT[A/G]CCAGGACCTGGCCCTGCACCTCCTGTTTTTCTTCTTCTCATCCCTGTCTTCTGCAAAAGCAATGCACGTGGCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTTGTGTGATGATGTCATCTCCAGGCAAGCCAC
ESTD-ACE	96 C T ---	---	GATCAAGCAGTGCACACGGGTCAACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCC[C/T]GTCTCCCTGCGTCGGGGGCCAACCCCGGCTTCCA
EST54419	88 A G ---	---	TGAGGCCATTGGGGACGTGTGGCGCTCTCGGTCTCCACTCTGAAACATCTGCACAAAATCGGCCCTGCTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTAC[A/G]ATCCTCTGGGAGATGTATTTGGGTTTAGCGTGGTGTGTTGTCTATCTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACACCATAGCCTA/GJTTCGTAGCCATATAATTGGTTGTGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGGCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGAGGGCCCTAGCCGGGCCCTGCTGGGCTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGTCATCGTGGCCATCGCC[C/T]GGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTGACTTCGCTGGCCGCGACCGACCTGGTGATGGGACTCCTGGTGGTCCGCGCGGCCCA CCTTGGGCG
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTGGTTCTA/GJAGCCCTCATCTCTTTTA CAGGATCCGCCACAGCATCCCACTGATCTGGCCTTAGGCTCTTCTTCTCCAATCCATTCCTCAAAAG GCTGCCACTGTGATCTTCCCAAGGTGATTCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCCTTCT[G/T]JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTTGTCTCAGCCCCACCAGAGAGTTAA CATTCTGCCACCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCCTTCT[G/T]JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTTGTCTCAGCCCCACCAGAGAGTTAA CATTCTGCCACCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACATTTTCTCTAATTAATTACATTAGTCTCATTAATCTGAAATATTAT TTTTTACA[G/T]TACCCTTTGATTATTTTGTATTCTTTGTAAAGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTCTATCACAAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGCTTTAIGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAAATTGCTTGATGAGCCTCT CAA[C/T]TCTTAACCTGCTGCCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAAATAAAGTGAAGAGGTAAAGAAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACCTTTTATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGCCCTGTCTTCCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAACCTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG[C/G]JAGCAGAAGCAGCAAGGAGAAAGGAAGT

WI-2625	98 G A ---			GGCAGTCCTGGCTAGTGGTAGACAGCACTGAAGGATGGAGGAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAAGGCTTATTTAGGA[G/A]CAAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACCAAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATTCACCTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTTCTCTTA	GCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTCCTCTCTTGACCTCTGACCTTCTCTAGTCTTCTTATAGG[G/A]ACCCCTGTGATT ACACTTAGGGCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GIGCCITT	GGCTTGCTCA	CTTGTTGAGGG AAGGTCTTG	CCATTGTTGAGGTTGGGTGGGTCACCTTGTCATTCCTCGCACTCAACAAGTGGCTTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAAATGCTTTCCATGCTCCGTTCTTTGAAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTTATGCCGC	TCAAGTATTGC CTTGTTGG	CTTGCTACCATGCAATTCACAGCATACAACCCTCAGTGAAATGCCGTAAACCCCATTAATAAACAT CTTGCCATCGAAGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACCTTGAAGTGACTTGGGA GAATAAGATTTTGGATGGATGAAAGCAGAGAGATGCTAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA	CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT
WI-1796b	29 A G ---		---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796	29 A G ---		---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGGCGTCAATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCAT TTT	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAAAGATGGGTGAGT AGTCACATTAGGTATTTTCCAATAA[C/T]AAATGCCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-1959b	87 C T ---		---	GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAATCAGTC[C/T]GGGTAACCTGAGAGTGGTTTTCACACCCAAA
WI-1973b	28 A G ---		---	GTTGTGCCTGTAGCAGACACAGAAGGCA[G/G]AGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1980b	140 C T ---		---	CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAATTGTATCTGTTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATTACCATAAAAAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAATAGC

WI-2015b	190	A G ---				TGTCAGATAGTCCGCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGCTTTTTTCCAACTT[AG]CATATACTT CTAATACCATAGAG
WI-754b	49	C T ---				GAAGGCACAGGGAGAAAGATGGCTGTCTATCTACAGCCAGGGAGAGAAAGC[CT]ACATTTATTGGTAA TCCTATAAAGTGCAATCTTTAAATTTGTATTACTTTAGA
WI-754	22	T C ---				GAAGGCACAGGGAGAAAGATGGC[CT]GTCTATCTACAGCCAGGGAGAGAAAGC[CT]ACATTTATTGGTAA TCCTATAAAGTGCAATCTTTAAATTTGTATTACTTTAGA
WIR-1b	56	A G ---				AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGCGCTG GAGGTGATGCTCCTCCTGAGGACATGGAGCTTCTATGTTGGAGCCCTCCCTG
WIR-1	56	A G ---				AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGCGCTG GAGGTGATGCTCCTCCTGAGGACATGGAGCTTCTATGTTGGAGCCCTCCCTG
WIR-3b	72	A G ---				TAATTTTAAATGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[AG]TCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T ---				TAATTTTAAATGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA[AT]GTATCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47	T ---				GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209	C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196	C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194	C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACAACCCAGCTGCAGCCAGAGCCTGTGTGCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191	A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCCGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
	177	C	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCCGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
	159	A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGT AGGTTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCCGTGGCTCTATGGAACACAC AGGTTTTACGTCCAG
	37	A	G	---	TAACCCCTGAAACTTTGTCTTCCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTTGGGCAG
WIR-6	63	A	C	---	TTCTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12	C	T	---	GGCGTCTATGACTATCTGGTCAATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46	C	T	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTGAGAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAC
WIR-2	56	C	G	---	TGTCCTTGCTTATGCCCTGCCCTCTTTCGGCTTGGCAGGATGATGCTGTCAATTAGTATTCACAAGAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAAGCTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAATGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTTCTAGACTCACCCTGTTCTCAGTCTC
WI-7069	93	G	A	---	GGTCATTTCCCTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41	A	T	---	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTTATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT
WI-18612	37	A	G	TGC	CTTGCATAAT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]GTGGCACTGTCCAAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAA CTGCACTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTAAACAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCTCCTACT
WI-18680	75	T C A	GCTGTCACCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAA[T/C]GCTCCGTTGTATATTCAAGAGGGGA
WI-18704	99	A C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTTGTGAGACACCAACCAAGGCGAGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[A/C]CCAGCAGGGCCCTTCAGCTTAAAGTCG
WI-18673	29	A G ---		---	TGTGGCAAACCTTGTATTTAAATTGCAAAAC[A/G]ACTTAAATTTACAGCACATTTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121	T C GGG	GTOGTGGGGTG GGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAGGATTCAAGCAACGATTGAGATT GTGTTCTCAGGAGGGCTCGGGCCAAAGTCTGGGTGGGGGTGCAGAG[T/C]GTGTCTCTCTC AGTGGTATTTGGGACC
WI-18533b	91	T C ---		---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCCGAGATTTTCTTCTTTATTT TATATTTTCATTTTTCATCCTAA[T/C]TTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G ---		---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCCGAGATTTTCTT[G/C]CTTA TTTTATATTTTCATTTTCATCCTAAITTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
D11734	83	A C TTC	TCATCTGATAC CTTGTTTCAGAT	AACCAGGATA AGGTACAACCT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTTCAGATTTC[A/C]AAATAGTTGTAGCCTTATCCTGTTTACAGATGTGAAACTTT
D49493	159	A T TCTGGGAATT	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT[A/T]GCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10030	98	T C TCTCAAGTCCC	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTATAGAGGAGACCTAGGAGGAGGTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT[T/C]TCATCCATACCACCTGCTGATTG
EST10052	24	G A GAGGCTG	GCTCACTTCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[A/G]GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGCTTC CTGTTGAGTCAATAACCTGGTGGAGTCAATCATGTGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---			CTTGGTAAATCACAGTTCTGTATTCATACAAAACCTTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAGATCCC
EST11048 0	61 T G	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAAATTTCTTCTGAAAATTTAGCTTATGAACCTCATTACACTGCAACACAGAGAGGAGCAC
EST11260 8	101 G T ---		---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---		---	TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCACAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGATTGAGCTTTACCGCCTTTCCCTCATCTGCTGGTGT[C/T]TTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	CCAACTACTT TGGAGCCT	CTAAAAACTCC T	GAATTCGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGAA
EST11772 6	74 A G ---		---	CCAGGAATAAAGAAAAGAGTCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCCTTCA[A/G]GACTATTTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---		---	CTTGTCATTATTTTGTCATGTTGTTCTTAAAGGCTTGTAAGATAAAGTGTGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCTCCACAGAACTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ---		---	GTGGAAAATTTTTTATCTGTACGCTCTTCC[T/C]ATTATATTTATCTTGCTTGATTCAGCACCCC CACCCGATTTGCAGGCAGTCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAGTCTTCT
EST12492 1b	95 A G ---		---	CCCCTAGCAATGACTTGGAGTTGTGTCCAAATACCAAGTTACATACTGTGGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTAA
EST12492 4	25 A G ---		---	ATCTTGAGGTTTCTGGGCTGTGAG[A/G]AAGTGACATCTTTTACTTACCACAGGTGAGGAACCTAT AAAGAACTGTGTAGAAAAGATATCAGGTGAGACTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAACTGGAGGCAAGTCCACAGGTCCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAATGCTCACGGGGGAAATGACCATTTTTAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCCTTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGC[A /G]TTGAGAAATACAATATTGAAGAAGAGTCACTGCCCTCTCTGGAAAAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTCATGAGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGGATGGGAATCCATGTGCTTTGCGTACTCCATCAGGTCATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCAGTTATTTCAACCAGAAATTTGTTTGGGTTTCA ATGATGTTTGTAGCTTTAATACACTGCACCTGTTTTTG
EST12949 2a	52 A G A T A C T G T T	GGCTTTAATCA TAACCTAATA	TGTGTCCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTGTTAAACAAACACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCCCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTTCTTAAATGAAGCATAATAAACAGTTAAAATTTCTCAGAAAAATCATCTATAGTTGA GTGTAAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAGCAGCTTCCCACCCCAAG CACTCTGAACT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTCTTTAAAATTTAATCGCTTTTATACAATTTGACACCAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTTGTCCTCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATAATGAAATAGTCT GGCCATT[T/G]GACTAACCCAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A A G A C G C	GCTCAGATGTG AGAGACGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C T C A G G C C T	AACCAGATTT TCTCAGGCCT	ACAAGAGGGTT TGACAAAAGA G	AAAGATATAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTAACCAGATTTTCTCAGG CC[T/C]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGTATATAACCA

EST13278 2a	51	A G G	CTTTCACCGAA CAATATTTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAAGCGTTTTACAAGCTCCAAACCTTTACCGAACAATATTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCACCCAGAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAATAATTTAGATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAAATCCCACACATTTTCAGTCCCAAGA[A/T]AACCTTCCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39	A G CTT	CAATTTT TAGA AGTTTGGGTTT	AAATCACTTCA TGGAATAATTCA G	AGCTCATCTGCAAGCAATTTT TAGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTCAGTTACTTAAAGACCTAAAGACAAAGTGATCATCACATATATTTTGT ATGTGTTGGCTTTT
EST13518 2	45	C G ---		---	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTTCAGCAATTTA[C/G]ACTTTTAAATTTACCTCA ATGTTCTCGGAGTCGTCCATAGTTTAAATGACTTTCIGCACCTTCCCTTATAACCTTGATTG
EST13522 8a	66	A G ---		---	CAGTTGGTGATTCTCAACTAGGAGCTATTTTGCCCCCATCCCCACCCGCGAGTGCTGGAGAC[A/ G]TTTTGATTGTCACAACTGCGAGAGGTGGTGCTACTGGAATCAGTGGGTAGAGGCCA
EST13568 6	69	T C ---		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C G ---		---	AAGATTACGGACCAATAAGAACTGCCCCCGACCCATACACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAGTAATGACTTTCTTGAACAAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A G ---		---	CCTCAACCATCTGTAAACCGAGCC[C/A/G]CAGTGACCGGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGGTCAGTCAGCAGGTG
EST14083 7	23	A G ---		---	CAATGGTGTCCTCATGTGAACATAT[A/G]ACCTATTTCATAAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGTAGGAGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATAATTTT AAAAGA	AATATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATT[A/T/C]TTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCTTCACACTCATTTTAAATTGT
EST14812 2	50	A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCTTTCAAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGGAGTTTGCCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGIGATT
EST14815 3	128	A T	CATCACCCACC ATACIGGTT	CGGGAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCCCCACTGAACCAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCATCACCCACCATACTGGTT[A/T]TTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---			TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCATAGCTTGGATATCTTA ATCTCTCCCTTTTGTGCATCATATAATCATATAGCCAAGGGACTTC/AJGGAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAAAGACAA AGACAAACAGA	GGAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACCTTTTATTAAAGACGTGAAAAGACAAAGACAAACAGAGGA[G/C]JAGCAGAGAAATAATA TCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGGCCAT	GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96 C T CACIGTAAGG	GGTGGGAGTCT	CTTCTATCTTT CTGTTCTCTCCA TC	CTTCTTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG[A/C]T]GATGGAGGAACAGAAAGATAGAAAGTTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G	AAAAATGTAAACCTTAGAGGTTGCCCTCTTTTGTGTCACCTTTTCTGAGATGTCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTATTAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---			CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTCAAGGCAACATAGGA[T/C]TGTGA CAGCACCACTCGGACCAAGGAGTGTGAAATCGTCACACTAGCGTGCCAGCCCCCTTTTCTCCTGGC TGCTCTGCCCTCCAGAGC
EST16088 8	89 G C ---			GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGACGCC TTTTCCAGAAAGGCCGCTC[G/C]GGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---			CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAGAGGCCATCCCTGCCCCCTTCTTTGCT
EST16100 1	24 C G ---			ATCCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCTCA GGGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---			TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCTCCAGGGA[A/G]TTGGCCCCGGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---			ATGGTATAACAAAATCAGTTCAGGTTTTTTTCTGAAACAAATGATCCTTTTGGTCTTTCCCGTGGCATG CTCCTAAAACAACTAAACACACCCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---			ATGGTATAACAAAATCAGTTCAGGTTTTTTTCTGAAACAAATGATCCTTTTGGTCTTTCCCGTGGC ATGCTCCTAAAACAACTAAACACACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATTCAAACGAACCTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTA[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGGAAGATAGTAGTGTGCAAAATAAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACACTGTGGTTCCACACGATTGTTCTTTTCATAAAGAAATAATCTAGTTG[A/G]GTAG AGGAAGGCACGTGCTCTGCGCCCTTCTTCGTTTCATATTTTATGTCACGTGCTTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAGTACGATCATCAAAACCATGGTCCATGCTCACGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGAGTACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGAGTACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGTCCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCTGTGGCTTGTCTCTGTCCAGCTGCTGCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTCTGTCCACTCTCTCTTCCGCCGCTGGGGCTCACCCACC TCTCTCTCTCAATC
WI-16824b	83 G A ---			GTCAACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTGTCCTCCAAAGTGGGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTCTG	CAGCTTCTGAC	GTCAACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/G]TCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTGTCCTCCAAAGTGGGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAATAAATGAAC[T/C]GGAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCCAACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTACAAAGACCTGTGCTTCAAAATGTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79	C T	GATACAGGC ATATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAATCCAGCAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99	A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAGACAATTCTCCCCCTTACCCCAAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTCTGAC/A/G]GCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTTT	AATGTTCTGAA TTGACCCAAAT TAA	GTAGTAAATGTTTCATCACTACCCGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C T	ACTTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTTGTTTGTATTTGCCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACCTTGGCCTGTG TTGTTCA/C/T]CCCACTGCCTAGAAAGATATAGACA
WI-16910	74	G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA/G/A]GTATCTGTTATAGAAACGATACTTCAATTTGGCCCTGAACCAAGTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAATACTACCACCTTCTCTCTGTCTACCCACAGAGCACTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC/C/T]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCCTCTGAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCAGGATT TGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGG/A/C]CCA CGGCAATCACATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG/C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGGACCA CGGCAATCACATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTTACTTTAAATGCACACTACATAACAACCTAATA/T/C]CTTAACTTGGTCCAACTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCCGT	TTGAGTGCCAGACATCAAGCATAGAGAGCAGTAGAGACTGAGGTAAATAGTATTT/C]ACGGCTGG AAATCAACATGCCCTCTTCTCTGTGAAGTTGTGAGCATGGAGCTGAGAAAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGCGCCCTCATCTGAGAT/G]GTG TAGGACTGTAAGGGAATGTGTTTGGGGTTAGGAA
WI-16992a	46	G A TC	AAGCACCAG AAGTACACTG	CACATTCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG/A]CCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTTGGGGTTAGGAA

WI-17010	23	T C	TTCAACAGGA AAAGCCATG	AATAACGGT GTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTT/CJATGACATTCAAACACCGTATTATTAGAAGCTCATTAAAT TGTTTAAATGCAGACAAAATCAAGGCTAACTAAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74	C T	CACTCGGCAC AGACAGAGT	GGGAGGCGCAGG GGTG	ATTCCGTCTCAAACAGCATCCAGGCGGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGT/CJTTGGGAGCCATGGGACCCCTGCCCTCCCCAGGCTTCTAAGTAACAACCT
WI-17040	94	T C A	AATTCTCTTAT CATCTCAAGCC A	GGACTATGGCT TATTCAGTGAT G	CACGGTTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAAATCTCTTATCATCTCAAGCCAGT/CJCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCC AAATCTTTCTCATATGT
WI-17044	47	G T G	GCCAAGGGAT TAACGTATAG G	GGGATCCOCT TGTTAAGA	TTGTTTGTGTTTTTCTCCTCCTGCCAAGGATTAACGTATAGG/CJTTCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAAATGGCAGGAATCGAAT CAAAAGAAAGCAAGTG
WI-17021	62	T A A C T C	TGGACTTGTCA GCCTATAACT A C T C	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCTATACTACTC/T/AJG CAGCTGCCACTAACTCTACAGGCACAGTAACACTACACTTTATACAGGAGCACATGCCAAAAGTGCCTGG GAGTGCCAATAAAATCAA
WI-17065	90	T C C T T	CCAGAAAGGA AAAGCATAAA C T T	CCCAAGAGAC AATGAAATCCT	TGTAAAATGTAGACATGGGGGAAACATTCGTAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTT/CJAGGATTTTCATTGTCTCTTGGGT
WI-17066	32	A C T	TGTACAGCCA ACATCACTGTT A C T	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAAACATCACTGTTT/A/CJATTCAGAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCAATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T G ---		---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCCTT/GICTACATAGGAGTATATTTGGCCAAAGACTCACCCTAGAAAGTGATT
WI-17104b	108	T C ---		---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCCTGATGCTTTGCGAGCTTTCCCATTCATCCCA AATCAGAAGCAGTCAGTGGCCCGTGGTTTCCAGACGGCTT/CJCTCTTTGTTAAGAAATTA
WI-17114a	37	T C	TTCCATCAAG GACTTTGTTT G	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTTT/CJGTCTCTTCACTCTGCTATTTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAAGAAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76	T G C T C T T	GATGAAATTC AGATAGTCTTC G C T C T T	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCCTCTT/CJCATATCTTCCAGGATCTGAGAAAGGGCCCTCTTTGTCTGCTCTAATTT
WI-17163	43	A G T A A C G T T	CATTCTTTGT AAAATAACAA T A A C G T T	CAGAACTTGC TTTTGCCTT	GAAATCGAATACGTCCATTCTTTGTAAATAACAATAACGTTT/A/GJAGGGCAAAAGCAAGATTCTG TAAACCAACATTGGAAAAGGGACACAGGGGAGGGGAGAGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

WI-17178	127	T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCCTCCAATTTCAATAGCTATGAGGATTATCAGTTTCATTTTCAGAGCGAATTACTGG
			GTGAGGAGC	CAACTGCTTC	GGCAGGGGGTTTAATATATCCTGATGGTTTAATTCAGTGAGGACTCCTTCATGAGGAGC[T/C]AGAA
WI-17180b	81	C G	---	---	GCAGTTGAAAATTGAGGG
			CACAAAAATA		TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATCCCAAGTCTCGTCGCACAG
WI-17180a	47	T C	TGCA	TGGCAGGAGAC	GCTTCAACAATTAC[C/G]AACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
			TTGGG		GGAGTC
WI-17156	54	G C	TCCCA	CAAGAAATAT	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACAT[C/C]CCCAAGTCTCGTCGCA
WI-17149b	79	T C	---	---	CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17149a	48	C G	CAAGGTTTGA	CCACGCACGTG	GGAGTC
			AGGAGGAACA	CATGA	TGAGGTAGCAGGGCATTTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATG[C]TTCCACAGA
					ATCAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
WI-17197	67	G A	CTGGGGCTAC	GCATACC	TAATATTTCTTG
WI-17198	38	A C	CCTAGTTT	ACTGAGAAATT	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACATCTCATGCAGTGGGTGGAA
EST18753	27	C T	GGTCTCAT	GCCTGA	ACCCAAATTGTCATGTTGATGAATACTACAAAGGATGGGAAAGAACACATTTTCTCACA
			GGTCTCAT		CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACAT[C/G]TCATGCACGTGGGTG
WI-17108b	74	C T	CA	CC	GAAACCCAAATTGTCATGTTGATGAATACTACAAAGGATGGGAAAGAACACATTTTCTCACA
EST19067	41	A G	---	---	ATTTGCTATGTTGCCCTGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAAGTAGCTGGGTAC[G
			CGTGACCATT	AAAAGTTGAA	/A]GGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAAGAAATATTGACTTTTAGATGCGCA
EST19067	40	A C	TTC	CCA	TGTAATTCAGTACTTTTCCCTCCCTTGCCCTAGTTT[A/C]TAATTTCTCAGTGGACAAATGGACAA
					ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
EST19125	28	A G	---	---	TTC
					TCGCTATGCTACCCAGGCTGGTCTCAT[C/T]TCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG
					GATAAGACACAACTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
					TTATTTTAAACATAACCAGATGCACCTTGGTTTTTACATTTCTCTGGTTGCCATTACGTCTCAAAGT
					AAACAC[C/T]GGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT
					ACACAAAAATTTACCATCGTGACCATTAAAGGGTATAGTTCA[A/G]GTGGCATTAAAGTACATTCAACT
					TTTTGAGCAACCCGCCATCACCATTATCATCCATCTCCGTT
					ACACAAAAATTTACCATCGTGACCATTAAAGGGTATAGTTCA[A/C]JAGTGGCATTAAAGTACATTCAACT
					TTTTGAGCAACCCGCCATCACCATTATCATCCATCTCCGTT
					CTGTTTCTCAGAGATGACACTGCCAACA[A/G]TCACAGATTTGTCATACAATACAGTTATGTATTGGC
					TATTCACAAATTTACAGTAGTGTGTTTTTCTCCTCTGAAAAA

EST20824 8	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGTT/GTJCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTT/GJGTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTGAGTGGGACCA
EST21904 b	128	G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGGTCTGGGAGCAGGTGGGCGAGTTTCACTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAATGTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T C	GAAGATCTGT CTGGCATTCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGCTGGCATTCTTTT/CJGTGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78	T C	AATTATTCTGC TATTCCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAACTTTAAATGTTTACAAAGCACCAATATTCTGCT ATTCCTGCCAAT/CJACCCGATCCTTCATGGTAGAGTATCACAAAGTAAAGTTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92	T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCCACCCTGTAAACAG TAGCATTCAAATGGTTTTTACTCTA/CJGTCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22311 9b	54	A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCAAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCAG
EST22311 9a	41	T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATAT/CJACATAAAATCCACCCTGTAAA CAGTAGCATTCAAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCAG
EST22319	19	A C	---	---	TCGAGGAGCTCTGAGGAGC/CJACCAAGGGAGCGTGTCCCAGGGCCCGGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTTAACTGT
EST22433 c	103	A G	AAGACATGTT CACCAAGTGA GAA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCCCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[C/G]TCTGTCAAGTTAAGCTGAAGCTGAAATT CTGGGAGCTTGACATGCTG
EST22657 9	71	A G	AAATGGATCC TTATCTGCACA	GCATGAATTTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAATACAATTTCTATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAATTCATGCAAACTGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGTT TCTACCCCC	TTGCCGTGTAA TTTGACTGTAA TG	GCCTTTTATTGTCCTCTTTTAAACATCAAAATGTTTTTATAACACACACTTGATCCTTTTGTCTACCCCCA ATTC/CATTAACAGTCAAAATTAACAGGCAATATAATAGTCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCAATTTGTTGTAATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAAATCTTTGCCCTTTTATGAGTTTGTGCTCTTTCT T
EST23021 0	108 T A	---	---	T
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAAA	GCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCAATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAACTCTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAACTCCAGAGGCAG[C/G]CTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G	GGCTGTTAGTT TTGTTTTTGTTT	TGCACCTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTTGTTTTTCTTTTCTTTT/GTTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCCTAGAGAAAGATATGAGGCCCGAGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCCGTCCCG CCAG	CCAGTGACGAG GCCGA	CTGACACGTCCCTGTGTGCGGGGTGTCATGTGCGGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTT/GTTCGGCCTCGTCACTGGCCTTGTGATTTCTGTCTTGGTTGGAAA TACCATCAGCCCTTCC
WI-17519	55 T C A	GTTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTGTTGTCCTAGCTAATGAATGCA[T/C]AGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	---	---	TCTTTGATACAGGTAACCAAGTTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTTT
EST25356 3a	26 A C	---	---	TCTTTGATACAGGTAACCAAGTTTTGT[C/G]ACATTATTTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAATCAACATT ACTACCAGTTATTGATAATGATAGTAGAACCCAA[C/T]TAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTTGATAA	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAAATGGGAGACAAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAATCAACATT ACTACCAGTTATTGATAATTC/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGTGGGAAGTAGGAGAGGCGCTACT TCCCTGTGTAAACACTCCC[G/G]ATATTGTGCTGATTTCTAGCTATAAGAAATGGGCGCCACTAAGTGGGTC

WI-17623	46 T C ---		---	TGTGGTTTTAATTTTCCCATATAATTAATGGTGGGCACATTT[C]GCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAATCTTTTGCCCTGACTTTTGAGTTTTTTGGT
EST26419 1b	46 T C ---		---	ATTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA[T]C]GGCAGTCCAAACTTCT TGGAGGGAAGTAATTCATGGTAATGTATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGCCC	ATTCATACAGAGATACAAAGGCAACTATGTGCAG[C]A]AACAACTCTGATGGGAGTCCAAACTTCT TGGAGGGAAGTAATTCATGGTAATGTATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780	69 G C ---		---	TCAGCTTTAATTTAAGGGACATGTAATAAAAGATGCATTTGACAGGACAGACACTAGTTCAAGC AG[G]C]AGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTCTGCTGTTCCATCTTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900	39 A G ---		---	TACTTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTC[A]G]GAGACGGGCACAGAACACACACC GTAGAAACACCACCACCATGCATGACGGGAAGCAGAG
EST27152	101 C T ---		---	CAAAGGATTTTATTTTCCCTAAAGTAATAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC[T]C]TTTACATGGTGTACTCTTTTCATGTACACAT CATCGGAAACACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCAA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAAT G	TTTTTGACCTTTGCAACAATTTAATAATTTATC[G]A]CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTTTCAGTATTTCTGTACACATTTCTGTTAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662	51 C T CTCCAGTCTTG	CACATTCTGTT CTCCAGTCTTG	TTATGGAAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTG[C]T]AGGTTACATAAG CCATTTCCATAAATTTCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788	100 A G ---		---	ATTTATTAGGGGTACAAATTCGAAGGTGGTAAGGGTGAAGGAAAGGCAAGGCGGCAAAATACAT TATTGAGCTGAAAACAACCTTTACATTCAAGGAC[A]G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAACCTTTCCTTCTGTTGGATCCCAGTGACGTGGAGTCAATCAGAACCCCACTG[A]GTACTT GGAGTACCCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAAATTC AATCTGTAC	TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTCGCCAATGTAAACAATAAATTTCAATCTGTACACAATC[G]A]AAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036	37 T C ---		---	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA[T]C]AAAAGAATGATCAATCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGACACACACCACGCCGTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAAT/AJATGGTATAAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAAACAGACGAAAGACATGAGTTTGTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGCOCTOCC TGTC	TGGGTGGCAG TGTOC	AGAAATGGTCTAGTAATGTTTCAGGATTCGGTGATGGGCCCTCCCTGTC/T/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACATTAAAGCATCATTTGTCACTTG/AJGCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTTAGAAGGACACCAGTCTTGTGGACTTAGGGCCTACCCATTCCAGCAGGTGCC/A/GJTTATTT TCACCTGGTTACGCTGTAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGGCTGGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAGAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATTGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA/G/CJAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATAATTCC/A/GJGGATTTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGACCCAGA GTTTCACAAATATAGGTAGC/G/AJATAACCCAGGTCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA/G/TJACCC AGAGTTTCACAATATAGGTAGCGATAACCAGGTCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG/G/AJGCCCTGTTTCCCTATACCCCAATATCATGAAT GTTGTTGCTTCTATAATGTTACGCTTCAAATCTTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTTGTCAAAA

EST31951 4	87	C T	GGGTTGTCAG CCAACA	CCCACCAAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACAATTTTCACTCTTTTAGCAATGACA TCGGGTTGCCAGCCAACA[C]/[GGAGGTGATTTTGGTGGGAATTC]TATCACAATTATCT
EST31968 8b	95	T G	---	---	CGAATTGTCCTCTTATTATTTGTGATTCTAGTAATCCTAAAGATTGGGGGCGGGTTACTATAAGT GCATTTTATAATGGGGAATTTCTGCTT/GJAACCTGCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGTACTGCTCCC
EST31968 8a	75	T C	GCGGGTTACTA TAAGTGCAATTT T	TGTAAGAAATCA GTGGGCAGTT	CGAATTGTCCTCTCTTATTATTTGTGATTCTAGTAATCCTAAAGATTGGGGGCGGGTTACTATAAGT GCATTTT/CJATAATGGGGAATTTTCTGCTTAACCTGCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCCTTCCAGACCTAGCTGGCTTTGTAGT[C]/[GTTCAGGCCCATTTGAAATAGCAAAAGGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCC[C]/G TCTGTATTAGGGAGCACCCCAAGCCAGTAACAATATGGTTCTTGCAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT[C]/GJAAGACTGGGATTAATTGTAGGAAATATTTACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G	CCTAAAGTCTG GGATGACTTTTC C	TGGCTTAGGT TCTACTTGATG T	AACTGTCAATTCCTAAAGTCTGGGATGACTTTCCTT/GJAATCTACATCAAGTAGAACCTAAGCCAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATTCAGCTAACTCCAAAGCTGAATTAATGTTCAATCT
WI-17860	121	T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAGCAAAAT[A]/[CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTTATAGCCT ACTTCTCAAA ATTGTT	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGTT[A]/[T]TTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACAATCAGTAACCTACCA
EST33301 4c	80	G A	---	---	GAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATGCCACGAGA[G]/[A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A]GTAAACAATGCAATATT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC GG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAATGAACAC[A/G]TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAACAAACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTTGA AT	AACTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTIGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A ---		---	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACCTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAACACACTTC CAGTGCATCAA
WI-17982	98 C T C C T A A A A G C	GGACCATATG ATATATAACT	CAGAAATTATG TGATAATAACT CCTCC	GGTACACAATTTTAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGACCATATGATATATACTCTAAAGC[C/T]GGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAAGTTTTTCATCA
WI-17993	118 A C ---		---	CTCAGTAACTCCGGTGTATAATCTGCCATTTTATTGATTTATGATAAAACAACCTCTCATTTGTGA AAACAGCTAAGGGTGACATCTCCAGACCCCACTGCTCTAAAGACGCCACCTCAGGTTGATGT ACATTTTGGAAATCCAAAT
WI-17996	84 A G A G G G A A C A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAACATCTCCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG[A/G]GCTGCCCATGTGCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G ---		---	ATTCCTTTATAAAACACCATGTCCCTAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24 A C ---		---	GCCACTGAAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G C C C C	CACAGCCCTGC C C C C	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC[C/A/G]TCTTGA GATTCAGAAATCCAGAGGGTGTCTCAGTCCCTGGTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67 A G ---		---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTTCTTTTCATGTACGAATC[T/C]TGGTTACACATCTT A/GJACAGCAGAGCTGCCCTGAGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTTCTTTTCATGTACGAATC[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A G A G A T A A A A	GGGAGTGGGG GAGTAAAA	CGTCAACCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[A/G]TGGAAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A	AGA	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGTGCCAATCATCTCTCAAAACCCCTGTGGTAGCTGCTAAGCTGTATTTTCAGA[G/A]GAATGTCAC AATCATACCAGTGGGAGAGAAAGAGTAGCACAGTGCTTATTAGGTGCCAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C	AA	GCATAAAATT TTCCAGTTGGT	CCCTCGGCACC TGCT	TTAGCACCAATCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAG[T/C]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAAGG CAGGCA
WI-18070	28	A C	GTGTAT	AACCCACTAC TTACTCAGAGT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT[A/C]ATATTAAACACATGAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTTCTGTACTCAGAAGCAATTTAGGTGGCAAAGGATATAA
WI-18080c	80	C T	---	---	---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACTTTTAT[C/T]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65	G A	---	---	---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCC[G/] A]TGTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41	T C	AGTCTCTC	GCAAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCT[C/T]TGTAAATTAATCTACTATGC CGTGGTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63	G A	---	---	---	GTGGCATCCTATAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTT[G/A] TGGCTTTGTTACACGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGICTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71	C T	---	---	---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGTAAAGCCCTTAGTGTACCTTTGGTATCCC TTC[C/T]TTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTAACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70	C T	TT	TTAGTGTACCT TTGGTATTCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGTAAAGCCCTTAGTGTACCTTTGGTATCCC TTC[C/T]TTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTAACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78	A G	---	---	---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTTTA GGTAATTTGC[A/G]TAAGAACAAATAAAGCATTTTAAAGTCCACTGCCGCCCTTAGAAACT
WI-18169	115	A G	GAAGCTC	CCATCTTTCCG	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCACTATGAAGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTTCCGGAAGCTC[A/G]TGGAGCACAAGCAGA ACTCGGTGGTAGAGTGA
WI-18190b	26	G A	---	---	---	TGAAAGAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGTCCCTGGAGAGACAGGACAAAATCAAGAAATGAGCTGGAGACATTAATCTCTGGCA

WI-18190	62	G A	---	---	---	TGAAAGAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAATGAGCTGGAGACATTAACTCTGGCGA
WI-18181	100	A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACACAAATACAAACAAACATTAGGAACAAAGAAATGTGTAATCCAA TGTTGAAACAAATATATACACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTTCTTGAAC
WI-18215	78	G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT CCCC	CCTCCCTCTCT CCCC	ATTCATACAAAGCATTTCTGAGTACAACTAGGGACAGGTATTTACAAACAAATAGAGCAGA GTTCTGCCCC[C/G]A]GTGTGCGGGGAGAGAGGGAGGATTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTC
WI-18232	60	T A	TGGTGTGATT GTGATACACTT AA	AAATAAGGT TTTCAGGGGT C	AAATAAGGT TTTCAGGGGT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAACCTTTATTTTGAATTTGAAGTTTGTCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76	T C	GGAAACTTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAACTTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTTCGTGGCATTTTCGGCAGAACTGGC
WI-18242	30	G A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC	GCTAACACTTC TACTGTAAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAT TGATGCCACAACTTATCTCACCATTCCTTTCAAGCAAGTGAGGTCAGAAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAAG
WI-18266c	119	C T	---	---	---	GCATCAGACATCACCACTCCTGAAACAACTTCTACAAGAAATTGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C	---	---	---	GCATCAGACATCACCACTCCTGAAACAACTTCTACAAGAAATTGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTATGCATCA TTTGTGCA	TTTATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAACAACTTCTACAAGAAATTGAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G	AA AA	GGAGAAAAGG GAGCAGAAGA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGGATATGTGGTTTAGTGTCTATCATTAATTTGGAAAGCTGTCAGCTATTGTTATTTC AAAT[A/G]TATCTTCTGCTCCCTTTTCTCCCTTTTCTGGGATTCCTCATTTCTGCAATGTTTATA
WI-18330b	66	A G	---	---	---	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGATAGAGCTGAGGAAACAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA

WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAAGGACTATGCAAAACCATAAAATAAAGAACATAAATTTTTTTGTTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGATACTGCAATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGA[T/C]TCTCATTGAGGCCCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104	G A T T	AAACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAAACAGCTTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCACTGAACCTCCAAATACGAACAGTGACGCTGATGG CCTGCAGTCCCTCTGCCGTGCTTGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTTGGGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCACTGAACCTCCAAATACGAACAGTGCA[C/T]GCTGA TGCCCTGCAGTCCCTCTGCCGTGCTTGCTCTCTGGACGGTTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G G C A T C A A	CCCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAGTCTCTACCGTGTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAGA TAATCCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCCTTCCAGCCCAAGTCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGGTACGCTCCTCTTAATGGCCTGAAGGTGATCTCCTTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCCCTTCGTGA[A/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGGTACGCTCCTCTTAATGGCCTGAAGGTGATCTCCTTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCCCTTC[G/A]TGAAGTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTGC	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTACGCTCCTCTTAATGGCCTGAAGGTGATCTCCTTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCCCTTC[T/G]GTGAAGTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGGTACGCTCCTCTTAATGGCCTGAAGGTGATCTCCTTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCCCTTCGTGAAGTGTTTCCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[G/A]GTAATTAAGTTTATTAAATCAGCTGACTTTAGCAATTGGGAGATTATTCTGGAT

EST38512 7	91 T	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAACTGACCCCAATTGGTAACTGTGTCTGGACTGAGAGAAACAATGATAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCGT/G/GCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T	CCTGCACTCC TAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACTCCCTAAAGATCTTTTC/T/CCCCCAAGTCTACAGAAATGGTATATCTCTCTGAAAAA AGATGAACGTCAATCAATGGATTGTGCTGCTCGTTTCAGCTTTGATTTTTTGCTTGAGAACCTTG TCTCCCTGCTGATT
EST38575 1	66 T C A A	GAACATCCCA TGTTTCTGTTT	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/C/TCTCTTATGTTTATACTACCTTCCCTTTCTCTTTCTTATACACATAGATTTTCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTGTGCTCCAGAGTGGTGCTCACGCCGGGGCCCGGTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTTC/G/GCCACCAATCCATTCCTCCAGGGG
EST38652 8	59 T C	TCTGAACCTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTTGTGCTGCAGCAGGAATTATTCAGTCTGAACTGGGCATTTCAA/T/C/GCGTG GTATTTTTTCTTTCATTTTGCAAGTAAATAATCAT
EST38654 5	42 T C	AATGGTCATTT TAATATATCA GTTTTACA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAAATGGTCAATTTAATATATCAGTTTTACATA/T/C/JAGATAGAAGATTAAAGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGCTGGTTCCAGCATATA GGATCCTCACTCACCTGGGACAGCCTGAGAGGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC/J/G/AGGCCAGCGGGATGTGTGCCCTCCTCCTCCCAACTCATCTTCAGGAACACGAGG ATTCTTGTCTTCTGGAA
EST38707 9	75 A G	TGACCTTGTAATCTTCACTAGAGGGGAGAAATCACTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATATGG/J/CCTTAAGTCCACGATGGTGACCTAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38759 2	86 A G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGC/T/AJTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCGCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGTGAC AAACAAACCAACATGGTGG
EST38815 4	91 C A CA	TGTTTATGAGA ACCCATTACA CA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTTATGTTGTTTCAACAAG TGTTTATGAGAACCCATTACACA/C/A/JAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T	CACGAGTAAA AAGAACTCA TGAC	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTTCCTCCAAGTTTGGGGTGTTCATATGTTATTGTTATTATTA TTCAACACGAGTAAAAAGAACTCATGAC/C/T/TTCTCCTTGGACTCGCTCCTCTCCCAATCTCGAT ACCGACTGCACGTGG
EST38865 2	72 T C	GCTGTAGAATT TGTGTCGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTACAGCTCATCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGTCG ATGCT/C/CTGTGTCCTCGTCCCTCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA

EST38878 9	47 T C	AACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCTT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATAATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTCCTCC TTATTCAATGTCTCATCTCACACATTCCTTTATTTTATTTTATTTTCTCACTTTCTCAAAATATCGGATTGTTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 GC	---	---	TTATTCAATGTCTCATCTCACACATTCCTTTATTTTATTTTATTTTATTTTCTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATTT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTTCTTTAT TTTT	CGATAATTTGAG AAAGTGAAAA CAA	TTATTCAATGTCTCATCTCACACATTCCTTTATTTTATTTTATTTTATTTTCTCACTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATTT TA
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTGTTG ATTCCTCATCTT T	GCACTAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G CAC	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAAACACTACACATCAAAACTTAGGGAAATGTGGTTAGTGTGTACGTTGAG GGAACTTATAACCTCAC[A/G]CGCTTGTTCACAAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATTCCTT GGTGGG	CACTGCAATCT CACCCCC	TAAACATTCCTTGAATTCCTTGGTGGG[G/C]GGGGGGGGTGGAGATTGCAGTGTCAAGATAAA TATCACAAATATATCAAAACTTCAAAATTTGTCTATGCTATTCACACACTGACATGAGCCACAAACATT CCTTCACAGGGACTGTAC
EST39002 0	42 G A	GGACCCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCCTGGGCAGATCCCGACCTTCGGTGAC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCCGGGCTCCCGCAGCTCGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCTTAAGTTCCGGGTCTTCCTCAGTCTGGATGGCTGTGTGGAAAAAGCTTGGTGAAG GCCTAAGGAATTT/GJAGGGGCAGGGGGCGATGCCCGCAGCGAGATGGTCTGTAAAGCCTGTGGGTC AAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTCTATCACAACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCTAAAT CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTTGTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGTATTTTCTCATTTCTCTATCAGGTTTCTGGTCTTTGTCTCAATTTTAAACACTT T/C]CTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCAGTT
WI-16406	24 C T	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCCTTAATGGCTACAGAAAGAGG[C/T]GGTTTATTTTCTTTTAAACACATCTGTTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA

EST39236	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCITTTTATTCATGATTTGTTTCATCTGAGAAATAAACCTTCCTGCTCTAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGTCTC TTT
EST39294	63 G T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTGCTGAGCCAGCAACCCCTCGAGTTACCCGGCCTTTTACCCACGCC AGCTCTGCTGTCTGTCAT
EST39366	72 T C	---	---	AGAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTAT[C/J]ACACTGAGAGGAAATGGAAAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371	86 A G	CATTTGGATTA GCGTGAGAGG TT	TGATTTGAGAC ATTTACACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAAATCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAAATGCTTCTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTTCCCTGTGTTTCTTT AGAGCCTTTTCAGCTATTTCCCTGTGAAGCAAACTGCAGGAAGGCTCCCCGTACTCCTCCCTGGAA G
EST39428	31 C T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCCCTGTTGCTCCCCACAATTTTGATT[C/J]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCTAGGTAACTTCTGTGGCTTTGGTCCACAGAGCACAAATTAAGAAGATCAGGTCT GGCTGTTC
EST39430	45 A C C	GGCAGAGGAA TAACTGATGTT C	CAGGGTCCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446	117 C T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAACTGAAGCTAGACACACGTCACCTTTGGAGAAATAACAGGAACCTATTTATAT ACGTAAATCACITTTACATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCC
EST39465	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGCAGAGAGGTGGAGACCAG
EST39501	81 A G	AAAGATTCTCT GTAGACATCT AACATTAG	CAC TTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGTGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG GCTATGTAGACATAAGA

WI-18387a	57	A	G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACAGJTITGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA
EST40601 9	78	A	G	GCGTGGAAACCT GAAACAC	TTCTTTGGAAGA AAGCGTC	TCCCAGGATGTTTATTCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACACAGGAGCGCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT AGGT	GCACACCCTTC ACACTGTTA	TCCATTGAGTGTATCACATCTTCAGGATAGGTAGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTGGGA CA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA[C/T]GTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTTCACAAATTTCTCATCAGTAAATTCA
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACACAAGAAATAAGGGAATAAGGGAACACAGAGTGAAATTAAGCAAAATCTTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAATAATCAAAT[C/G]CTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAATTTTAC TC	AGAGAGACAACAAGAAATAAGGGAATAAGGGAAGAA[C/T]AGAGTGAATTAAGCAAAATCTT GGATTGAGATTCATTAAACAGGAAGTTTCTCAAAAATAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	CACCCTGTCT AGACAGATTTC A	...	AGCTGATCAGCTGTCTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCTGTG CTAGACAGATTCAATGCACACAACAACAGGAGG[C/G]GGGGTCAACGGGGGAGAGCCCAAAGAC TAGGGC
WI-18425	81	A	C	CACCCTGTCT AGACAGATTTC A	OCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGTCTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCTGTG CTAGACAGATTCA[C/T]GCACACAACAACAGGAGTGGGGTCAACGGGGGAGAGCCCAAAGAC TAGGGC
WI-18449	129	C	T	CTTTTGGCTCT AAGTGGGACT T	CTCCCTGACT GTATCCAGA	AAATTGAGGTCCGGTGGAACTATAAAAGGAAAGAAAGAGAAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTTCAGTTCTTCTTTTGGCTCTAAGTGGGACTA[C/T]TC TGGATACAGTCAGGGGAG
WI-18457	120	T	C	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCTGATGTCTGTGTTTGTGCACATTGGGGCCACAG[C/J]AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462	39	A	G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTGTACACCACAAATGGCAGAGGTGA[G/J]TAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGTGGGAGG[C/T]GGT CACTCCCATCGTGCCCTGGCGTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	G A	AACAATGGT AGTGGTATT	CGTGTGCATTT TCITGTAATCC	CTAATGAGATGAATACATGAAGCGGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAAATACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGAGGGCC[C/T]GGCGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTTGG ATGGTGACTT	GGGGAACCACC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTACCAGTGCTGAAGAAAGTGCTTTCGTTTTAAT TGCCAAAGCAGGGATGTGGACATTTGGATGGTGACTT[C/C]CCTGGGTGGTCCCATAGATTACCCAT TGCCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAATA CATTTGGGTT	GATTCATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAATCTCCTGAATGTCAAAACAAAGAGATAAACTACATTTGGTTTTGG[G/T]AAGTCCCTGTAAATGATGAATCAAGAATCCTCAAGTCTGTCTTGCCACCCCATTTAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAATTGTC TTCCACAAAACCGTCCCTGGTGCCAAAAGGTTGGGAA[C/G]TGCTGTGTCGGTACAAAAGTAATT G
WI-17690b	79	A G	---	---	ACAACATGTGAAGAAGATATGTTGTCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[A/G]GATTACAGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGTCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTT[G/A]A TTTGGCTTCCCTATAGATTCAGGACCCATAACTCTTGTTCACATCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCTCCAGATTATTTCTGAAGTGGAACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCTCAAA
EST51717 a	39	C T	---	---	GATCCAATCTCAGTGTCTAACTCATCTCCAGATTAT[C/T]GAAGTGGAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCTCAAA
EST53012	97	C T	TGGTCACTTTG GGGCC	GGCTCTGCCCA GGCC	TTCCAGGTTGACAGGTTTTATTCCACCCCTTCCATCCCTCCATGGCCACCCAGGAGGAGGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATTTCTGT GGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCACATT TT	AACTGCAAATAACAAAACAAAGTCCAAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATAITGTTGAAAGCAGTCACAATGTAC[A/G]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAA CA	GCCCTTTCTAA CAATAAATGCT C	TTTCGAAATGCTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAAGGAGATGGCC

[illegible]

TGR- A003P30	117	C G ---			ACAAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TGR- A004S34	156	C T A			GCTTGCTTTTATGTTAGGTTCCGGGAAAGGAGGGGCTGACAACCCGAGACATCTGGACACCAGC AAGGGTCCAGGGAGGTTTGCAGAACTTCTTTGTCCTTGGCTAACAGTCTGTGACAAATAGCCA AACCTCCTCATTCCTATAAA[C/T]CTTTAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C ---			AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT[C/A]AATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAACAATATGACTTAGCAAAAGAAACAATATAG
TGR- A004T44a	69	G A TGA			AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCAAATGAT TGA[G/A]TATGATAAAGAAATTTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAACAATATGACTTAGCAAAAGAAACAATATAG
TGR- A004V08	60	T C GGCATTCTCTT			CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAACAGGCATTCTCTTA[T/C]GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACITTAGGGGACAAATTTGGCAGTAGCTGTCAAATTTTC AGTAGCTGTCAAATTTCAA
TGR- A004V26	125	A G ---			TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAATTATCCAGAAATAATCTATTGAATTGA CTGATTACAAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TGR- A004V28 a	29	A G CGATCTC			CCAGGCTATAATGTTGTGGTGGCATCT[C/A]GCTCAGTGCACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACCTAATTTTGTG TATTTTATAGTAGAGACATTGTATTTTATAGTAGACACAGG
TGR- A004X20	25	T C GA			TAAGTTTCCCTTCTCTGTAGGA[T/C]GTCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTTCATTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCTCT
TGR- A004X30	26	T C CCAC			TTTGAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACTTGTAAATAAAATAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCCGAGCTCCTTGATTTCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102	T G ATGCAAAACT			CACGGTATATGCCCTTATATATAGTATATATACAGATCGTACACAATATATTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[T/G]TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTTCTTCATATTCATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCITTAGTGATTTAAGACTG

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X57830	106	G C C T	AGT GGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTCGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/C]TATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA TGGATC	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATGACTGCTTTTAAAGAAATTTTGTATG GATC/T/G]GATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCCCTTGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATTCTTTCAGAGCTAATTAAGCCGAAGAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T ---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCTCTCATCACAG/C]T]TAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACGTGTGAGAAATGGAAGAGCCCCCTCCAGACCCT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G ---	---	---	ATGACCAAGCCACACATTTAGAACTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCCAGAGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGTATTGACTGCATGAATGC/A/ G]GTGCGTGAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ---	---	---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGAACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G ---	---	---	CTCCCTGCCTCCTCCTCCTGCTGTGATGCTCCGCTCTCAACAGCCGAAACCTGCTTGCAATGGGGG GAGGGGGCGTTTC[G/A]CTTTCCCTTCTTCTGGCTTCTCTTATTCTTCCACAACCAATCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCCTCAGGCCACCTCCTGTCTCCTACTCCTGTCTGCTGGCTTTT CTGGA
D31762	82	G A ---	---	---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCAATTTGAGCTG[T/C] CCCAGGCTCTGTCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATAACTCATTTCTATTAAATACATT GCACCAAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAAGCTTCC TTT
D37931	64	T C ---	---	---	

D63807	101	CT	---				CAGCAGGACTTCAGTGCAGTATCCCTGCCTTCAGTCTTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCCCTGTTCCA[C/T]GAAGAGGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCTGTTCTCTCCCGTCGGCTTCTCGGTGCTGGAGGGTGACCTGTCCAGATGAC
D90145	21	TC	---				TGGGAACATGCGTGTGACCTC[T/C]ACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACCTAAATTTAAATTTAATTTAATACTATTTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTTCCCTGTCCTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	TC	---				ATTATCAGCTCTCAAAAATTTTGGTGTGTGTTAAGTACTTTCTTATTATGAGCCCC[T/C]GAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT
EST16668 5	71	CT	---				GCATTTTAAATTCACATTGAATCATTTTACTATTTATGATGTTTACATAACAATTCAGTATCATTT ATG[C/T]GTAGATTTTCAGATGTAGTGTGTCATACCTGAGCACTTATCT
EST16904 7	57	CT	---				ACAGACTATCGCCAACCTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTTATTATAAATAGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTTAAACAT
EST21863 9	49	AG	---				TTTTAAGTACCAGGCACTGCTGGAACAGGATGAAAACTGATACACC[AG]GTTTACTACTTACTC TTCACCTTTCAAACTGATCCCTTAAAGACTTCTACTTAGCAAA
EST21885 6	80	GA	---				GGCTGTAAGTAGAATCAAGGTTAAGAACATTTTATGCATTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGG[AG/A]TGTGACAGTGAGCAAAAACACAA
EST22623 8a	26	AG	---				ATTTAGTGCAATGACAAAGCCCAA[AG]AGAACAGAGGATCAATAAGATTGAAATGTATTACC TTTCATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644 2	98	AG	---				AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTTTACAG[AG]AATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31	TA	---				CCTCATTTTATTTAAAAGACGGACATAAAAA[T/A]TATACAAACAAAACCCAAAGTCACATTTTCAG GAGGTAAAACCTAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106	TC	---				AAAGATCTGGCATTATTCACATCATTTCTAAATAATTTTGTAAATTTCTTCCATGAGTATTTTTTICA TGTCCTAAGCATTTTAACTATCATTTTAGCGTAAATACC[T/C]GAATAACCCCATAGTTACAGAATTGG GTCGTGTAAACCTCAATT
EST24308 3	45	AG	---				TAGTTTAAATTTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT[AG]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73	GA	---				CTTGAACCTTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC[GA/T]GCCCTGACCCACATTTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST25089 6	25	TC	---				TATTGTTGCATTATCAAAATGGTTA[T/C]AGTTTTCAAATTAACCTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAAATGTAGTTCCCAATCGTTAGTTAATGCTACATT

EST25476 9	33 G A ---	---	AATGATCTTTATTTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAACCAACACACA AGAGGTCCCTCTTGCTGCTTCCATGGACTGTGGCGGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCAATTGTATCTTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	AGAAAATAAGGTGCTACAGAACTCATG[T/C]GATAGCGCTTTCTTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTATCATCACACACACTGTGCCTCTAACAAACAACACGGTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAATTGCAT[T/C]TAACATTGTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---	---	GTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCIGGGAGGCTCAGGAA ACTTACAAATCA[A/T]GGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGGGGAT
EST30226 5	25 A C ---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAAATTAGCTATAGCTACTGCTACTAATTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAACCTGTTGAATAGATAATGGCCAAAT ATTACAGTTTCTCACCTTCCCTATGAATACTGGCAGCTGTTTATTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTTGTTTCCCTCCAAATCCTAAA[A/T/C]GTGTGCTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TAGGAGTTTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATTT GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGCAGAAATACATTGCTCCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTTACTAAGAGAAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCCACAGCAAGTATATTTATTGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTACACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTGAATCCTCTT
EST33488 7	90 A G ---	---	CCTTGGGGGAGTTTAAAGCCAGAAATGTGACAAAGTCACCTTACAGGAAGACTGGAATGTAGCCATAG TTGAACCTAACATCGTCTATAG[A/G]JACCATTTCCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTTGAACAAACCTTTTATAAAGAAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	AAAAATGCTATTTGAACAACATTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTTAAAT AACATCAACTACAAATGACITTTAGAAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAACATAGGACTGGTTATTTCTTGTTTTGAAAAAATTATGTTGCCACTTCCTATTGTTTTTAAAAATGA TCATTTAAC[C/T]TCTTTGAACCTACAGCCTGAATCCCC
EST34739 3	97 T A ---	---	GAAATATCCTTCCAGTGGCAGGAAGTGAAGACTCCAGATCAACCAAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCCCTTACAACCTCAACTACTGCAGAAATTTCT TGTTGTGCCTCATAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCAGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTTCTTAGTCCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---	---	GGAAAAATGTTCCCTTTGCAAAACAAGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTTCTGG[T/G]GGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	GGAAAAATGTTCCCTTTGCAAAACAAGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGTCTTCTGGTGCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T --	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	TCTTTTCAAATTTTGTAGTGTAGGCATTTAATG[C/T]TATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTGTTCCATTTTACTTTAGTTTCAGAACITTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACITTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTCCCTCTCTGAGGTTGGCACCTTTTCCTGTTGTG ATGTGCAAAGTGTGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTCCCTCCAGTAGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATATTAAACTGAGGGAACAACGGTGTGCTGACATGGCAGACATTTATTTCATGGAGA AGTTCCCTCCCATGAAACCAAGA[C/A]CTTGTCCTCATGATAAAGTGGAGACATAAGAAAGCCAGGT ATATAATTAAGCCTGTGA
EST36301 4	93 C T ---	---	CACCTGTTCAATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTGCTCAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	GCCATCAGCCCAACAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGTCTTAGTCGT

EST36620 6	50 G A ---	---	---	GACTTTATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	---	CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCTCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACCTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCTAATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACITTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	---	ACTGTCGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAATAATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAAGTACATTTTATGATGCAGTTT[C/G]GTTA GGGAATTAAAGACAATGCAG
EST37054 3	88 T C ---	---	---	GGTCTCACTCTCTGCCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCAACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	---	AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCCAGCAAAATTTCTCAGCTTATATTTTGAAAGTC[T/G]CAGGAGAAAAAATGGGTCC
EST37284 2	93 G T ---	---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	---	AGATGGGGTCTTGTAGCTTGTCTGGGCTGAACCTAAAGATATCCTCTCCTCAGCCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCTCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCTCTCACATAGCCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	---	GTGACATCATGTCTCTTCAATGCCCTTTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAAATCACAGTGTGTGTCTGCA[G/C]GCTGTCTCCTCAGGCAAGTTGCTGACTTCTCTG TGTCACGG
EST37376 8a	41 T C ---	---	---	GTGACATCATGTCTCTTCAATGCCCTTTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGTTCAAAATCACAGTGTGTGTCTCTGAGGCTGTCTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378	9	63	T G	---	---	ACACACAAAAAATGGTGGCAGAAAATCTGGAAAGATTCTAATAACCTCAATTTCGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAAAACACTGTGCTGACATGATTAGCTT
EST37452	4	46	G A	---	---	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613	6	34	A G	---	---	CTAGGCATGGGCTTTTACAGTCATTTATTTACC[A/G]GTCATGAATTCATTAAAAACACACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCCTGGTTTCATGGATCTTCCATTCTAA
EST38025	4	56	T G	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTA[T/G]TTATCTCA ACAATCTTGAAAGGGTGGIATTAATTTCCCGTCTTATAGGTGAAGACICTGAGGTTTCAGAA
EST38068	6	57	C T	---	---	TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/T]CGCATGG AAGAAGCTCTCCTTTTAAATCCCTAACCTCTCTTCTTCTGGGAAGACAGAACGTGCACAA
EST38420	6a	100	T C	---	---	TAAATCAAGGCCTCTTTCAATTAACCAAAACAAAAAAGGGAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTATCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCT TATTCATTCTCCTCTCTCA
EST38950	5	25	T C	---	---	TTTATTTGCAAAAGTAAGCAGCGG[T/C]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053	6	90	T C	---	---	TTTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[T/C]AAACAAGTTACTGAATATTTTTCACCTCGTGGAGTTG
EST39331	1	70	G C	---	---	TCCTTCTTGCTCTAGCACTCAGACCCACCAAGAAAGCCTGGAAGACCAGCCATGGAAGGAAAGTA TGC[G/C]GTGTTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544	7	31	C A	---	---	GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548	4	37	T C	---	---	TTCTAATAGCATGCCCTGTGACAGGGAACTAAGCTC[T/C]TCAAAATAACTGAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549	1	42	A G	---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTAGTTTGTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACTTTGGGGAG
EST40579	1	81	A C	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCACTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGGATTTAAATACGGAACAAGGTCTTCCAGGAAG
EST40584	3	68	A G	---	---	TTGTATGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTATGTCACACCC A[A/G]TCTGTACTCCACAAATATCCTATGTTTTAAGCT

EST51340	51	G A	---			GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGACACACCATCCATTGTCTCTTTCAAACATAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134	T C	---			CATGGAGTAATAAGAGCAGTGGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA T/C]TTTCCCTTGGTCTCCAGTGAAGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63	T C	---			CTGAACCTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTTCTCCTCATGTGAAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCT TAGTAAAGTTTCCAAACAATAAGAAATTAATGACACATTTGGTAGCACTAATATGGAGATTATCCTTTT ATTGAGCCCTTTTATCCT
L18877	69	T C	---			TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAAGGOC C[T/C]ATCCATTAGTTTCCACTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTTATCTTTGTTTCCCTGTTGGA ATTGTTCAAAATGTT
L31848	36	T C	---			GCTATTTTACATATCCAAAGCCCTTTAGGGCTACAG[T/C]CTCTTGCTCTGGACCCGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAGAAAGGCTTTGGCCCTGGTGTGGTGGCATAGGCCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137	G C	---			GGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGAGCTGGGCAACACACGCTCCCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123	T G	---			ACTTGAGAAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTGTCTTTTGTATTTTGTATATTT[G]CGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGTGGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173	G A	---			CAAAGTTGTCTCCTGCCCATGAGCACCCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGTCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAAAGCATGGATTGTGTTCTCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAGCTGGAAGAGAGCTCAAGTTTTTGGTTTACTTTCAGAA[T/C]GAAGAACTTATTTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCCAATGCTCCAAAACACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GGCACAGTCCAAAATACAAATTGGACAGAAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGGTCCCTTTTATAAACATTGGTATATTTCATTTCATGCGCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	---	TAGGATCTGTGCCAGGCCATTGCGACCCAGCCACCACCTCCACCCCTGTAGTGCTCCACCCCC TGGAAGTGGGCCCCCACCTGCGGGAGGCCCTCCCATGTGCTG[T/C]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCCTTTGTGCTCAGCAGGGCGCTCGGCCCTCCCTCCTTCTCGCTTCTAATA GC
M21539	114 T G ---	---	---	TCACCTCGTTCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAA[T/G]GTTTCTCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTATTCCCTGACTTC CTGATTTTCTCTCAAGTGTACCTACTAAG[A/G]GATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTATTCCCTGACTTC CTGATTTTCTCTCA[A/G]GTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTC[T/C]G]CAAAATGTTTCTCCTCACCC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTATTCCCTGAC TTCCTGATTTTCTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGCAGCTGTGAGGGGCCAGTCACAGTCCAGCAATTCACAACCACTTGA[G/C]AATGCT TGCCAAAGCTGTTTAAAGCCAAGAACACCCTTCTTTGTTCCAAATTAACTCTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTTACCCTCACCTGTGAGGCTGACGGGA[G/A]GAACCACTGCACCACCGAGAGGCTGGG ATGGCCCTGCTTCTGCTTGGGAGAAACGCTTGTGCTGGGAAGGGCCCTTGTCTTGTCAAGGTTG CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	C T ---	---	CTCCTCCTTTATTTAGCATGGAGGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTTAAAAAGATCTTTTACAACTTACCTTGTTAAGACAAAATT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAAATTAATCTATGTCAATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39	T C ---	---	GAGGCCTTATGAGGTCCTCTACTTCAGGAACACCCCA[T/C]GACATTGCAATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAG TGGGGCTCTCTGAGTCTCTGGCCCAAGGAAGCAAGCAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGGCGTTGTATTTCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCCGCCCTTCCAGCCCTTCCCGAGCCCTCCTCTTGTCTTCTTC ATTCAATCAACAAATTTGGC
U10694	20	C G ---	---	GTGACATGAGGCCCATTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTCTGGTCTCTGTCTATTGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTGTTCAATGTTCTTTTAAATGGTCAGTTTAAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---	---	AAAAAGGACTCTGGTTCAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCCAAGAGAT[T/C]TACCGTGGTCTTACTAAAGTACATATCCTAACCTTGG GGTTACCTTCAGCA
U15555	187	T C ---	---	TTCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T C ---	---	TCCAAATTATTGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAACGTCCACGGGATTAAACAGAACGTCCTTGACAGACTGAGCGATGACACCCACAC[T/C]TTGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58	T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCAGCTGGGTAGTTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTTTATTGTTATGTCCCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACCTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGCAATTAGCACTTCC AAGCTTTAGTAGAGAGGCC

U25975b	164 C A ---	---	TCAC TGTGTGGCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143 C G ---	---	TCAC TGTGTGGCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61 A G ---	---	CAGGGAGAGGTTATTACAAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCTGGTTGATTTTAAAGTAGTTCCCTATTTCTATCCCCCTTAAAGAAAATT GCATGAAACTAGGCTTCTGTATCAATATCCCAACATTCTGCAATGGCAGCATTCACCAACAAAA TOC
U28413	29 C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCCCTCATGTTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTCCTTGATCC CAGATGTTGTGGCTGGGAAAGCCCTCATTTGCTACAGTACAAGTAACACAAAGTCGTTGTACCTCAGTT G
U30884c	89 A G ---	---	TAGGGGTAGCATTAAAGATTACAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	TAGGGGTAGCATTAAAGATTACAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCACAGTTGAACACAAGT GCTGTCA
U31216b	78 A G ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTATCAA[A/G]CCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCACGCCGATTGCTTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G/A]TCATCAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCACGCCGATTGCTTTAGCCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTCCCTCTCTCTTGTACAAATGTCTAGGTCCCACTGCCTGCT GGAAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC IC/TTCCTCACGCCACAAATCTGGTCCCTCTCTCTTGTACAAATGTCTAGGTCCCACTGCCTGCTG GAAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---	---	ACGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCCCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGGTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGTCTTGTCTATCTGTTGGGACGCTGCTCGAGAGAGGCCGAGAGGCCGCGAGAAC ATGCCAGGTGTC
U37690	54 A G ---	---	GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCC[T/A/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGTCTT
V00540	39 T C ---	---	TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAAACATCATGTTTACCTGTGCAGGCACACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---	---	TCAAGAGGTGACTGCCCTTGTATGATGGGATGGAGATGAATGACTGGTTTTTACTGGGTGTAA AACCACCTCTGAGCCTCTCTGAGACCATGTGTTTTAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCCTAGAAATTTGGATTCACTCTGTTTTTTCATGTCTCTCCTT GTAAACCTGAGATCATCAG
X52011b	148 C T ---	---	AGGAAGATCCCACCGACCCCTTCCCTGGCCTAATCCTTTAGATTAGTGCACATTACATTAACATTTAGGA ACCCAGACCCGAAAAGTTGCTGAAAGGGGAAGGAGACACATTACAAAGAAAAGTTGCGAAAATTGCG AAATCTGTGTGCA[C/T]GCTCAAATGAAAACGCCCTTTCGGCTTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A/C ---	---	AGGAAGATCCCACCGACCCCTTCCCTGGCCTAATCCTTTAGATTAGTGCACATTACATTAACATTTAGGA ACCCAGACCCGAAAAGTTGCTGAAAGGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAATT GCGAAAATCTGTGTGCACGCTCAAATGAAAACGCCCTTTCGGCTTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

1282	130 C T ---			GTGCGATCACCACACAGTCTAATTCAGATGTTTTCATTACCCCTAAAGAAATCTTGACCCATTAGCAATTATTCCTCATTCTGCCCTACCCCCAGGCCCTACTCTTTATCGCTATAGATTTGCC[C/T]ACTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACCTGAGAAATAATGTTTTCAGGT
6810	68 C T ---			AGTATCACACATACCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAAACTTTA[C/T]AGAAGCATTTTAAATTTACAACACAAAGCTCAAAAGAACCTACAAATAAGTCTAGTCTGTTTACGTGCCAAGGATAAGGCTGAACAATAAATAAACCCTTTAAAAATGTCTATGAACAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGAAATATTTTAAAGGC
6817	118 A C ---			CCAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGGCCCTGTCAGATCGGCTTTTGGTTGGTCTTAG
6819b	212 C ---			CCATTTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGTCCTTCAACAGTTTTCATATACAAAAATTTTCTGCTATTTTGCTTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---			CCATTTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGTCCTTCAACAGTTTTCATATACAAAAATTTTCTGCTATTTTGCTTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---			CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G/T]TATACTATGGCACCAATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAAAGAAATGAACGTCCTAGG
6972b	149 G T ---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCCTGTACCT CTGGTAGAATTCCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAAACTATTGATTATG CACAATTCAGA[G/T]CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G ---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCCTGTACCT CTGGTAGAATTCCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[AT]GA
7598i	192 G T ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTG[A/G]GATGCCCTT TTAATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCCAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTAATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGIGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACAC[C/G]CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGIGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATT[A/G]TATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGIGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCTATCTTCAAGGTCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAAATGAATGGGTAGTCT[A/C]TCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTTGCCAGCTCTCCTGTA ATACTTT[A/T]ATGAATGGGTAGTCTCTATCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTATTTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAATGGGTTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAATTCACACAGAGCATGCACACACAAATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAAACGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCATT TG[A/G]CGCAAAATCCACTTTGCTGTAAACGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTCAGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCAATTAATCGAAAAAGAAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTCTCTAACTCAG

WI-18562	29	G A ---	---	CTAAGGAAAAATTAATGATGGAATATC[G/A]ACAAATATTCACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---	---	ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTGTAAACCACAGTGTCTCGCACAGTTC AC
WI-18683	22	C T ---	---	TAAGCTGTTCCAGGACTGGACTC[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGTCCACCCAAA CAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75	G A ---	---	GACTTTGGTGATTTAATTGCTTTTCCCTTAATATAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTTCCGTGAGAC
WI-18563	94	A G ---	---	AAATAAAGTTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGTGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---	---	GTCTATTTCAAATTAGCTAGACCCATTTCATTCTGTTAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---	---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---	---	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---	---	TTTATTACAATATTAGGTGGCACAATAACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAAATA
WI-18715	76	G A ---	---	TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCCACCCC
WI-18535	107	G A ---	---	GTAAATAAAGTTTTATTGGCACAGCCACGCTCGTTCATTATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGTCCTCCCGTG
D17525	107	C T ---	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGGCGGTGAC TTCATCTCTTCGAACTTCAGTTCTTCATAAGATGGAA[C/T]GCTATACCTTACCTACCTCGTAA GTCTGATGAGGAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAAGGTCGATGTCTACCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTTATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTTATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTTATAGTAA[C/T TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGGTGGCACCCTCCTACGTCAACATGAAGTG TGTTCCCTTCAGTGCACTCTGGGAAGATTCTACCC[C/T]GACCAACACAGTTCCCTCAGCTTCCATTTCGCC CCTCATTTATCCCTCAACCCCGCCAGCCAGGTGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAAATGCAACTGTTGATTTCCTCAACATGGCTCACAAATTTCTATCCAAATCTTTTCTGAA GATGAAGAGTTTAGTTTAAAACTGCAGTCCCAACAAGTTCACTTCATATATAAAGCATTATTTTAA CTCTTTGAGGTGAATATAATTATATTACAAATG[G/T]AAAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	-- -- --	---	ATTTAGTGTCTTTGCGTTAAAAATCATTTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTAAATCACTGTAAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTGTAG GCCTTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTATGGTTA
DWU-447	85	A G ---	---	ATTTAGTGTCTTTGCGTTAAAAATCATTTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTAA[G]ATCACTGTAAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTTATTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTG TTAGGCCCTTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTATGGTTA
DWU-476	63	C G ---	---	GTAAATTCAGTTTTTTCCAGTTCCCTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGGTTCTTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67	A T ---	---	TCATAAGGCGAGTATCTCCTCTAGCTAGTGCCCATACAGAAATCTATCACCATACAAAATTTAA ATTGTCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGGACTTTGAGCTTTAACTTTTAA
DWU-512	131	A G ---	---	AAATCCAGGCAATTCGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAAGTGAACTTGCTTTGAATATCCAGATGTGTTTGGTC[AG] TGCGTATGGCAGTGAGCAGGTATGTGTTTGCTTTTGCTTGCACTGAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTTATTCAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A C ---	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTTCTTTTCAGCTTGTTTCTATACITTTGTA ATATACAGTTTTTTGTAAACCATATGATTGA[VC]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTCTTGCTTTTACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTATCTCTAAATTTCTAGTCTCTGATTTC
DWU-59	94	C T ---	---	CATTTCTTTGTGAAGGTAAATGGACTCACAAAGGGAAGAAACATGCTGAGAATGGAAGTCTACCGG CCCTTTCTTTGTGAACGTACATTGGC[C]TGAGCCGTGTTTCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTTAACTTCCAAGGTGTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATG CCACACGGGTAAAGACTCTGAGTCTAGTGGTTAAGC
EST11	68	C -- ---	---	CTTGATCATGGGGTGGAAATTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T ---	---	CACACTGGCATCTAGGCCCTTCGCCCTGCATTGCAGAAAGGAGAGCCAGGTCCCTCGGAGAA[C]TJG CTGCGTTCCCGAGCCCCACACCGGCTTTGCCACACACAGGCTGTTGAGGCAGGAGGTGGTAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCTCGGGAGAGGAGCACCTTTAGAACATGGAA AAGTGTGGTCACTCCCATCATTTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40	A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[AG]GAATGAAGTGCCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAACACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97	T A ---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATTTCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C ---	---	TTCCAATGTAAGAGTCAAGTACCAAGT[T/C]AACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATTTCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T ---	---	TGTAAGGTGACTTCTATAAGCTTCCCTAAACGTCAAACTTTCAATTTACTGAGATTATTTTCAGGCCAAT GTGT[C/J]TGTGGGTCTGAGATTGATTATCAGCTGGGTAAGTTAACCTGTTCCTGTTTCA

WI-18063	105	G A ---				AGGCTTTAAACTGATAACAATTGGCTTTAATCACATACAAAACTCTGCACCTTCATTCCCTCCTTC CCATGTTTCTGATTTGATGTAACTTAAATTTGT[G/A]TCCCTTAAACAATATACTGTAGCTGCA
WI-18078	86	A T ---				AGTTGAAAGATCAGAGAGGTTATGGTGGTAGCTGAACCTCAGATTCAAACCTGGTCCAGTGIG TTGTTTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---				CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCCCTTTGTTAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTT[C/G]GGGCTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T C ---				GCAATCTGTACAGTTTGGTAGTGGTATTACAGAGGA[T/C]TTGTAAATGGATTGGAGTACTTAC CACTATTTCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTGGTTCTT
WI-18142	66	T G ---				TTCAAGATAATTACAATTGGAAGGGGACCAATAATTCACCTTTTAAATCGAAAATAATCTATATAC[T/G]CCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAAGACACCAAAAAGAGGAAAA
WI-18178	68	T C ---				GCATAGGGTTGAGGGGTGTACAAGAGGAGAACAGATTTCAGTCCATGCTGGAGGTTAGTCTGGGG GT[C/G]GGGGGATGGACACACAGACACACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T ---				TCAATCTGAAAACCTGCTGTAGCCAGCATGGGT[G/T]GGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACCCACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---				ACAGATGTCAGTTGTTGAATTGGCCCATTAAGATGGGGCTTTTCTTTGTTAAAAAGTCATTCCAAA AGGCTTGGCAAGAGTTTGTATACACGGAGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAGGTGGGCTGTC
WI-18261	26	G A ---				GATTTGAAGGGATTGCTTTATTTAAC[G/A]TGAAAAGCGTGATAGAGGAACCTGTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAAGATTG
WI-18268	88	C T ---				TAGGAGGGAAAAAGGAGGTGGCTGGCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCTTACTTCCCCATAGAT[C/T]CCTGACAATGTGCTGCAGAAAGCCTCCAACTGGAAC
WI-18299f	107	C A ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTGGTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAATT[C/A]TTTTGCCCAATTATTGACATATTCTG CAG
WI-18299e	101	A G ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTGGTTGCCAATTTTTT ATCTATTTG[G/A]GTCTGAGAAATCCACAAATTTTGAAGAATTCCTTTTGCCCAATTATTGACATATTCTG CAG
WI-18299d	77	G A ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTGGTTGCCAATTTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAATTCCTTTTGCCCAATTATTGACATATTCTG CAG
WI-18299c	67	T G ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTGGTTGCCAATTTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAATTCCTTTTGCCCAATTATTGACATATTCTG CAG

WI-18299b	52	G A ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTG[G/A]TTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAATTAATTGACATAATTCTG CAG
WI-18299a	48	C T ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAA[C/T]TTGGTTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAATTAATTGACATAATTCTG CAG
WI-18307	76	G A ---			TCAACTTGTAACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTCCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T ---			TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAGCATGCAGAAAGTG
WI-18350	48	T C ---			ATGAAAGTCACCTTCAATCATAAGGGTCAAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAAGTCA
WI-18395	77	G C ---			TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTTCCCTGGAAAAATTTGAAGAATAAATTG ATTATTCAAG[G/C]JTGTCATTGGTTTATACATATCTCCTCTTCTCTTAATGCAAAAGCTATG
WI-18398	62	G T ---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACCACTCAAGGGT[G/T] GATAACATTGCCAGTATAACCATAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	C A ---			CTCGTTGGTATTCTCTCATCC[C/A]JTTCCTTTTCGCTCTTTCTAAAATTAAGAAAGCAATGGAATT TTAAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACCTTATCAACTTGACAAAAGTC AATGAAAA
WI-18409a	20	C A ---			AAGATGGGAAAGAGGAAATC[C/A]JTTCCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAACTCTGGGGCCAGAGCCCCCAAGTGCTA
WI-18442	62	C T ---			AAAAAGGAAAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGGAACACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	G A ---			TTGATGTTAATACTGTCACTCTGGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18489	102	A C ---			ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAACA[A/C]JGGTTATGGCAATAGAGGTGAAAAAGAA AGGCCATATAA
EST5b	93	A ---			CTGGTGGGAGGAAACAAATTGTGGTATATTTCATACAATGGAAAACTCTTCAGAAATAAGAGGAA CAACCCACTGAATCACACAACATGGACAAATCTCAAAATCATTATGCTGATGGAAAGAAACCATTCA TAAGAATACACAGTACAT

WI-20103	168 C T ---				TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCAATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAAGCTGGGTCTCCCA[C/T]TTCATCTGCTCAAAGCTTCTTTGAAGGAGC TGGTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---				GCCTTACCCATTTTGCACATATATACATATGCCACCCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116 A G ---				TGGTTACAAACCTAAGCCCATATACAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTTAACTGAGTTTAAAAAAATAACAATGCAATTTTTTA[A/G]JACACTGTTTTTGA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---				GTCTCAAGGGGGAGAAACTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGAA[A/G]AAGGGAGTTTCCACGCAGCGGTGGTGAGC TGC
WI-20613b	156 A C ---				GTCTCAAGGGGGAGAAACTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAGGGAGTTTCCACGCAGCGGTGGTGAGC TGC
WI-19984	47 A G ---				CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATA[A/G]TATAACATTAGAAAA GCAAAATTCITTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---				GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAATGGAAGTGGTATCAGGCAATA ATTGTTTCCCTTGGAACCTGCAACCGACTGTCCATGCTCTGTGGGACTTACACATTCAGTTTGACAG T/C]TGAAAAACCAACTGGAGCTGCTTTTCCAAAGAAATGTTCTGTTGCCTTCAATAGGAATCCCATG TTATTTCTTTCTTGCCCTTAAGCTCTTATATCTTTTCAATGACCTAAGCTGA
WI-18846a	49 G A ---				GAGTGCCATACCTTCTCCAGGCCCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACCTCCCATCCCGTAAGACCTCCTTCCCTCAGCAGGCCCAACATG GCCAGACTCCTT
WI-18959	123 G A ---				AGCAGTGGCCTTATTGCATCCCAACCAACCGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAAGGC ACAGCTAATTCTACTACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCAC[C/G]A]GGAAGCCG TCCTGGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAATCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTTCTTTGCTTTTGCCTTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAAATTCATTGAGCAGTTAGC[T/C]CATTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAAATCCCCCATCATTACTGGTAAAGCCCTCATTTGAAATGTGTAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAAATTGGTTTACGGCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGC[G/A]TCTGGCTCTAATTCACAGTGTCTTTTCTCCTCACTGTATCCAGGTTCCCTCCCAGAGGAGCCACCAAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[G/A]TATTAGAAATGTACCATAATTTTGTAAATTAATTTATGTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTGGCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA[G/A]GTGACGATGATGTGAATATTAGAAATGTACCATAATTTTGTAAATTAATTTATGTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTGGCAA
WI-18771b	75 G A ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCCTAGAAATGTTGGG AACAGAA[G/A]AAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCCTAG[G/A]GATGTTGGAAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAAATTTGAGACGCAATACCAATAGGATTTTGGTCTTGGTGTGTTGTATGAAATTTCTGAGGCC[T/C]TGATTTAAATCTTTCAATTGTATTGATTTCCCTTTTAGGTATATTGGCTAAGTGAAACTTGTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCCTGTAGCCCCCTCACCCTTCCCTGTTTTCACCTTTTGCCAATGTA[C/T]ATCGGGTTTGGTTTCTTGATTTAAACGGTTGTGGTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCCAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTGCTCTCTCTCATCA TCATTTCCCAACAACATCCTCTGCCA[C/T]ACACACAACAAACGTAAAGTTTCATTTGGGCAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCCGAGTCACCAAGGCGCTGTCTGGCCACACAGAGGGCTGCCGTGTGGAGCCTGCCCAACGGCCCCGGCAGTCCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTGCGGGGACCAGCAAAGGCCCTTCTCACTGGGTGGTCAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCAAGAAATCTTTTAAACGACTGACCTTCCCTTAAACACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCCGAGTCACCAAGGCGCTGTCTGGCCACACAGAGGGCTGCCGTGTGGAGCCTGCCCAACGGCCCCGGCAGTCCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACT[C/G]CGGGGGACCAGCAAAGGCCCTTCTCACTGGGTGGTCAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCAAGAAATCTTTTAAACGACTGACCTTCCCTTAAACACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGGAGAAATGTTGTAGGGGTTTATTTTTTAAATAGTGTTCATAAAGAAAT/ GACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCG[G/C]JAGAATGTTGTAGGGGTTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTC[C/T]JGGAGAAATGTTGTAGGGGTTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCC[C/G]CTGGCTG TGCACATTCCTCCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCGGAGAAATGTTGTAGGGGTTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCCCTGTAGTTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTGTAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTTAGAACCTCCTATTITAA[T/C]JGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTTACACACCTACTAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAAACCC AAATGGCTAGAAC[A/G]JTGTTTAAATTAATTTCACAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTCTTCTTCTTAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAAATTACAACTAAATTATTATGCCCTCTCTCACAGTCAAAAGGAACTGGGTTTGGT TTTTGTTGCTTTTATAGATTTATTGTCCCATGTGGGATGAGTTTAAATGCCACAGACATAATTTA AAATAATAAATTTGGGAAAGGTGTAA[G/A]ACAGTAGCCCCCATCAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCCTCAGAAACTGGAATAAGCCTTCGAAAAGAAATTGTCCTTGAAGCTTGTA TCTGATATCAGCAGCTGGATTGTAGAACTTGTGCTGATTTTGACCTTGATTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAAATACCCTGTACATACTTTGAGTTCAA[C/T]CTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAAGACAAAGTCTGIGGCTTG

WI-19042	193 A C ---	---	TTTGTAGATTGTTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAAGTCCAAACAG ACACAAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTTAATACTATCTTCTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGTCTTATTATAAATTCATTAAACACTACAGGTGTGAATGTTAAAA TGTAAGCCCTCCAGTTTCAATTTTCAGTTATTTTCTGAGTGTGACAGAGCTATTTTCGCACTGTATTAAAT GTAACCTTATTTAATGAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCAGTGGCATGTTTGACT
WI-18851	90 T A ---	---	GCTTCAATTGGCGATTGATTTCAGTGCCCAATGTAAACAGGGTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCCCTTATTGTATTCT[A/G]TAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGC[T/C]GGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTCTGCTGTCCAT[C/G]ACTGTCTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAAGTGTCTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTGCGTGAGGACGTGGCATCTACTACTACGTACGTGGCATAAC ACATCGTGTAGCCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTG
WI-18908	70 G C ---	---	TGGAAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGTCAGTA TGG[G/C]TAGGGAAACATTCCTTCATCTGAGTCAAAAATCTCAATTCCTTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCAAGCTTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGTC CCCTCCCTTACGAACACAI[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACCG[C/A]CCTGTATGCCGCGAA ATATCCCAAGCTTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	TTGAGGAGGTGGGTGAACCTGCTCCTTGGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCC[T/ C]CGGGCTCTTCTGGACCTTGACCGTGGATACCAGGCCATGTGCCATGGTATTTGGTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCTGTGGCTTATGTCAACCAACAGAGGGTCTCTGAGAAGTCTGGTGGCTGGGATGCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGAAGCAG/A/GTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACCAGGCACTACGGCTTCCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAAAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTAAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC/A/CTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAAAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTAAATATGACATGGTAGAGAATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCG/A/CTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCAATTTATTTCT/C/GATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCGCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAACCAAGGCAAAATATACATATACCTGAATATAAGTAACCTCAAGCCATG AGTATAAGATTAAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCCC CTTAGGGTGGGAGCTCTTCC/C/A/CTACCACTCCCAAGGCAATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTAICTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAACCAAGGCAAAATATACATATACCTGAAT/A/JATAAGTAACCTCAAGC CATGAGTATAAGATTAAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTTCCCTTACCCTCCCAAGGCAATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTAICTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCTCCAGCTCTGTCATCTTGTCTTGAGGGTCTGTGTTACGGCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAAGCCAGCTCTCTAGAGGCTCCA/G/A/JCAGAA CTGGACCCCTTAACTACAAAGGAATCTTGGATGAATATTTTACGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGAGCCCTTTCAGCCCTTTCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCCTGCTCTCCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGGTCA/T/G/A/JGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACTTTGTTTGT/C/JCATGTTCAAAAAAGAGTATTAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGCCACCCACTCTTCGGGCATTGCTGCAATATTCCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCT

WI-19766b	93 A G ---			TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTC[A/G]GACAAACAGAAAGGCACACCAAGCCTGAACCCCTCCGGACAACAGCAGAGTTACCAAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCAACCCTCCTCCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---			TGGCCTCAATGACTGGTACATTGGAGAAGCTG[A/T]GCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAACAGAAAGGCACACCAAGCCTGAACCCCTCCGGACAACAGCAGAGTTACCAAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCAACCCTCCTCCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---			CTTCCTCTGTTGGCTTTGCATTTGTGCGATTTGGAAAACCACCTTGAAGAAGGACTTTCCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGAGCCCTTGAAGTGA[C/G]AAAGCTTAGAAAGGAACTGAAATTGCTTCTTTGAATATGATTTAGGGCGGGCGTGGGTGGCTCAGGCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---			CTTCCTCTGTTGGCTTTGCATTTGTGCGATTTGGAAAACCACCTTGAAGAAGGACTT[G/T]TCCTGCACAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGAGCCCTTGAAGTGAACAAAGCTTAGAAAGGAACTGAAATTGCTTCTTTGAATATGATTTAGGGCGGGCGTGGGTGGCTCAGGCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---			GGGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAAGGATCGCACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACGGACAAAGGTAAATCACAGCTAACAAACGTCATGTTGGCTCACACGTAAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGCA[C/G]TTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---			TGTTTGAAATAAAATTTCCATGGTCTTAATTGAACGTGATGTTACTTCTTTTAGAATATCCTTTTTCATTAAATAAT[T/C]TCTAAACCACCTCTATGTGTTCAACCCTTCTGTTTAACTAAGATATGGGTTTTGAAAGGCCACAAAGTCACCAGCTCCATGAAGTGGCGAATTGGTCTTGTGTTGGAAAGCTCTCCAGGTGTTTCTCCAGAA
WI-19909a	29 T C ---			CCAGAAATAAAGCCTGAATATTCCTTTCT[C/T]TAAATAATAATTTTCTCTTCTTGTCTTCCAAATAATCTTAAATGAACCTGTTCTAGTCTATTTTAAATCTAGGCAATTATAACACTACCTAGGCGGGTTTTTCTTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---			TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGTCTTAGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTTAGCAGGAGGCAGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGGTAAATATTGGGTGACGTCATGCATCCCCCATGCATTGGTTT[G/C]ATGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C ---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGTT/CJGGA AACAGTAAAGCAAAATTACCCACACAATTAGGAGGAATTTATTTTCAGACATAGGATAATTTAAACAT CACTCAAAATACCTGGAGCATGATTCAGCAATAAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCAATGGAATCCGTATT
WI-20895	107	G C ---	---	TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTTCCCACCCAGGAGCAACACTTGACTTCATTAAAGGCAAA/CJCTTTACTCTGTACTTTTTCCTC CCACATAGTTTAACCCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72	T C ---	---	CCTGCAATCACAAAAGTGGAAGTGTGATATTTTGAAATCATACTTGTATTTAACCCACCTTCAGAAA TTCTA/CJAAACACTAGCAACTTCCCTTTTATCAGA
WI-19415c	161	A G ---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAAAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTGCAAGATTCCTTAAGTAAGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/CJAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAGGCTTACAAGTTTACACTTCCCTG
WI-19348c	103	C T ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCAATGGCGGTGA/CJTGTCCTTCTCCAGGCTCATATGGATGTCCT CGAGGTTGCACAGGGAAGTCTGCTGCTGTGTAGAAGCTTCTCC
WI-19348b	98	G A ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCAATGGC/CJAGTGACGTCTTCTCCAGGCTCATATGGATGTCCT CGAGGTTGCACAGGGAAGTCTGCTGCTGTGTAGAAGCTTCTCC
WI-19635	98	A T ---	---	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTTGTAGGCCATTGTACACAATG TTAAAGGTACAGTAAATAACAGTATTAT/CJATCTTATTGTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCAGTACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCCTT T
WI-19641a	46	A G ---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/CJATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTTGATTTTGATTTTACAGAAGATGTCAGGGCTATCTCATT AGTTATTAAATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGTTTAAATTTTAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/CJAGGGTAAACCAG GACTATTGCATGAGCATTCCTTAATACGTAATTTGATGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T ---	---	TCGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGATCACCACCTGTAAATCTAATAGT GAAAGGCAAAATGATGTCTCAGTATCAGTGTGAAACATTTTTC/CJCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCACACAGTCAAAAAACACAGCC

WI-19673a	35	G A ---	---	TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]TCACTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACTGTAAATCTAAT AGTGAAAAGGCAAAATGATGCTCAGTATCACTGTGAAAACAATTTTCCCTTGGACCAGCTGAAAAGAA TCTTGAGGAGCCTGAAGCCTTCAAGGTCACACAGTCAAAAAACACAGCCC
WI-19724	35	A G ---	---	TTTATTTGGGAAACAAGGATTGTAAATTTGGGTAA[A]GJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACAGAGATTTTGGTTTTTCTCTT
WI-19307	196	T C ---	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCAACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTGCTTCATGAGAAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAGAAACCAAGCAATGTATTCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---	---	CTTCCCTCATCCCTCTTCCACCACACCATCCCGGAACAAGTGTCCAGGATTCCTGCCCACTGGC CATTTTGGAGTGTCC[A]TJTTGGGTAGCAATGTGAAACCACCAAGGCCCTTTGTGGAGAAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTAGGGGCCCTTGCACCTTGTCTCATAGCGGAGCTCG ATCTCCTCATCATCTGGACAGGTGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122	C T ---	---	CAATGGACTGAATGAGTGCCTGGTGGGTGGGCGCACACACACCTTCAATACACGTCAAGGTGCG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCCTGAGACGCCACAGAGAGGT[C/T]TCTTCCCTG ACCCAGACGCACTCACGAGCCAGGTCTGTTTTCAAAACTGCATTTAACCTGCGCCAGAGAGTTCA CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---	---	CACAGCATGGTGTAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCAATAAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTTAGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAACGACCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCTCAA GTGATGCCCAACAGAGCTTCTGAACCTCCTCCTGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---	TTGGTTGGATACCTTGTGGAAAAAAAAGCAGTTTTAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATCTAGCACAAAGATTTTCTGTAAACTAGATTATGTTGTAAACTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCTATTCCAAATCTATCTTGGCTCTGAAAAAAGTGCAGA AAGGCACCTTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATCTT
WI-20218	26	T C ---	---	CCACACACTCTGTTTTATAAGCTA[T/C]JAGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAAATAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGAAATGACAACAGCCACATGTGCCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATCTACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---	---	CAACCTTTTGGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAATAATCTCCAGGCTTGATTGGGAGGGGCTGGGCTCTACCCCTTCTCTTTCCA TCCAGTCTATTGCCAGA[T/G]CCAGAGAAAGCGGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTACCTTCTGTGACTCCTCATGCTGGGACTTGTCTTTCCGGG

WI-20361a	192	G A ---	---	CTGGGAGTGCTGACCTAAGTGACATTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAATGGCTTATGCAAGATGACAGAATATGTGAATCTGATTGTCCAGAGTTACACTCTGCACTCCAAAGCTACAACAGTGCCACAGCTGAGAGGTTCCCTATACTTCCTACTACTGTGACAAATTTAGC[G/A]ATCCTTCAAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75	A G ---	---	GAGCCAAACCCAAACAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCTTCAGAAATT[A/G]TCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCAAAATTCATCTTCTCAAAATTTTAAATTTGTTTAAATCCCAAAGGTGCCTATTGAATTCCTCAAAAATAAACTGCCTATCAGGTATCATACCTGCAATGCCTCTAATATCTCTTGATTAT
WI-20588	133	G A ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAATAGTATACAGCAATCTTCACCTTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTTCCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTCAGG
WI-20593	79	A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTGCTGTACTTCAG[A/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAAAGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCCCTTCACCAGACTATCCAGAGCCATTCCATGGGGTATTTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCTCTCA[T/C]ATGTATCTTGTCCTGCTGCTTTTAGGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTTCTTTTCTCGTGATCAGTGAATACTGATCTATTCTCTGGCTAGGTCAAATTTACAAAATTGCCATGGAACTGAGCAAAAGGCCACGTGGGATAAAATCACTCACCATCGACGCCACCAGTATT
WI-19066i	239	A G ---	---	TGACAAAGGAGAGAGGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTTAGCCAGTCCAAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTACAGTACCATTGCAAGGCAAACTTTTCTTAAACGCCCTTCACT[A/G]GTTTCTTTTAA
WI-19066g	184	C T ---	---	TGACAAAGGAGAGAGGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTTAGCCAGTCCAAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTC[T/G]GGATGCTCAATTACAGTACCATTGCAAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066f	148	T C ---	---	TGACAAAGGAGAGAGGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTTAGCCAGTCCAAATCTCTACGAGGAACTGGCATATGTTCTTGCGT[C/T]GGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTACAGTACCATTGCAAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA

WI-18919	26 C T ---			TGGATGAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCATTTTATACTTCACCTTTCTCTACAGTG TTGTTTTGTTGTTGTTGTTTTTATTTTTTATACTTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI- 18741c	64 G A ---			CTTTCGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 18741b	38 G C ---			CTTTCGGTCAAGGCTTTGGACATCTCTTCAGTCATCAG[C/G]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 18741a	23 T G ---			CTTTCGGTCAAGGCTTTGGACAT[G/G]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 19179a	170 G A ---			TCAGAAGCAGACATGGCATCTGTTCCCTGCTTGGTTGTTGGTTGTGTACCTTTCACGAGACCTGAATT TTAGAATTGCCAGTGTCTGCCAGAGTGAGTGAGTGAATTCCTCTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCTATAACATATCAACCA[G/A]TAGCATTAAACCATTTTATTCCTGTCTCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ---			CCAAGTTGCATCCATGTTGATTTTCTGATGAGACTAGAGTGACAG[T/A]GTTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAAAATGCAGCTGC ATAATTAACACATTATCAAAAGTCCCTTACAATTTATTTCCGCAGCATGTCAAGCTAAGTAGACCCA ATGGGAGAGAAAATGCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---			CTGTTGAAGGCTTCCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTTCTTCCCATTTATGGGCATGAAATATGTGTTTAGAATAAGGAACAAGCATATT CCTTGCCAAACAGCCTCACTCTAAGAGGCTTTTGTGCTGAGTCAAGCAACACTTGCTGCTGTGCC CTTGAG[G/C]TGCAATTGACCTGCTCTCACTGGTAAGTGACTTGGTGGC
WI- 20014b	214 T C ---			TTGAAATCCCAGTCTCCTGGCCCCCAGGCAGGGTCTGTCCACCATAGAATGCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTTCAGAGCAATGTTTCTGTATTCTGAACTGGAACTGAACCAAGTTTGCTTCTCTCTAGTCACC AAGCATACTT[C/T]CTGCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---			GTCTCCCCAGAGTGCTTCTGCACCCCGCCCTGTCTGCTGTAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGGCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCCTTCTCAATACAGCC[T/C]G CCCTTGCACTCCCTATTTCAAAATAAATTAGTGTGCTTGCCTGTCTGT
WI-19135	20 G A ---			CAGTTACCTGCTTTGCCCTC[G/A]AAGTGTCTCAATTTGTAAATTTAGTATTAACCTGTGAAAAGT GTCTGTAGGTACGTTTTATATATAAGGACAGACCAAAATCAACCTATCAAGCTTCAAAAACCT TTGGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAACCTGATTTTATTAACCT GCTTTGCCCATATAAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGGGTGCACCTTGACCTCTGAGGGTTGGGTGGAGGGGGAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTACGCCGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACTCCTGGCTATCTCAGGGGAATGGGGAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGTCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCCAGCCTTTCTAAGG CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTTGAGCTATCTATCTATATTCATTTATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAG[C/A]ATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTGTCTCTTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA CTJGGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTGTCTCTTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTAGGAAAGTGAATGCAGGTGAGAAACCTAAACATGAAGGAAGGGTGCT CATCCAGCAACCTGTCCCTTGTGGGTGATGATCACTGTGCTGTG[C/J]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCGTGCTCAGCTCTCTGTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCTCAGTCCCCAGATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTTACACATGGTGGAA[A/G]GCTTCAATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCGGTCTGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCAGTTTAGTTTGGGATGATTTGATTTCTGTGTGTTGATCCCATTTCTAA CTTGGAATTGTAGCCTCTATGTTTTCTGTAGGTAGTGTGTGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCCCTAAAGGGACTCTGCCGAA[C/T]TTTACACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTACACTGACGTGTCCAGAGCAGCATT
WI-19117	134	A G ---	---	AAATAATGCAACGCAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTCTTAAGACATTTTTCATTCATGAATATTTCAAGTTTTTTCATACTGTACA CATTTCTTAAACACATGATACCGCAGCACTGAAATGAATGCCGAATTG

WI-19134c	263	C T ---			CTCCTGTTGCTGACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCCTCTATCTTCCCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGTGAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAGCAC TTCATCCACTTGCTCCTCCTCTACCCCTCGGCACCCCTGGGTGGGAAAGGG
WI-19134a	162	T C ---			CTCCTGTTGCTGACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCCTCTATCTTCCCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGTGAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATTCAGACGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAG CACTTCATCCACTTGCTCCTCCTCTACCCCTCGGCACCCCTGGGTGGGAA
WI-19224	112	C T ---			GGTTTCACCACTCTTCCAGGGAACCTCCGATGAAGTGTTCACACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTTC/TTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAAGTTGTTTCATAATCCAGCAGGCCAGAAAGACTTCC AGGGAAACTCATTCAAGGAGGTGAAATGATGGATGACTCCTCCAAGATGAAAA
WI-19201	179	T C ---			GCAGCTCCTAAGGACCCTGGCCATTAGCTCTTGTCTTTTGATGGCATTCTCTTCCACCTTGTCTCTC CTTGTCTCCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCAGCTGCC CTTCCGCCCCACACTTTCCTGCGAGGTGCACCCGAAAGGAC/TTC/TGGGGGATAAATTCAAAAA GTGTGATGTGCTGCTCAGAAAGGTGAGACTCCATGCTGCTTGGCCTCAA
WI-19034	45	T C ---			GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAA/TTC/TACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTTACAGTGTCTGCTGTTTGAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTGCAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25	C G ---			TGTTCTGAGTCACGCTGAGGAGAG/C/G/CTTCACTCAGGAGTTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTTCTTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGGCTAGAACTCCTGTAGTTTGAAGTCAAGGGGAGAAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---			AAAGGAGGGAGAACTCTTTTACATAAATGCCCTTGCAATCATCCTCCAGTCCCCTCACTGGGGAA/A/ GIAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G A ---			AAAGGAGGGAGAACTCTTTTACATAAATGCCCTTGCAATCATCCTCCAGTCCCCTCACTGGGG[G/A/A] AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T C ---			GGCAGCAGCTTTTAAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGGCTTC/TJAAGATCCACAATTGCAAGGCCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121	C T ---			CAGAGGGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTGCGCAGGACAGAGGGGGC/TTC/TGGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87 C A ---			ACAAAGAAATGGAATAGGTTGGGAAACTTATCTGCATGTACAAAGTAATCCCCGTAGATAA GGAGAGGCAACCCCNCGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATTATATCTCTTTGCAT CAGAGCTGGTGGAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCTTCGATAAACCTCTCTTTGGGACTATGAGATCATCAACAGATGTGAAACGAAAGCA GTGATTTTCAGAAACCNCTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTTGTGTGACCACCACCTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]]GCCAAAATCCCTCTTGCTTCCCTTGCTAGTCAGTCCCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117 C A ---			CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCACACCTTTC CTGGGTGGTTTCTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCTATTGTGGGAAACAAACAG[C/T]TTGGGAAGTAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64 T C ---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTACACGGGTGGGAGACACAA[T/ C]GAGTAATTAACAACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG GGGAGGAGGGCGTCTTICA
WI-22585	56 A G ---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAAATG[A/G]CAGAAAGC AGCAGTGAAAGTTTCGGAGAGGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGATGGGAAATTTGGC[A/G]TCTGTGTAGAAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTTGCTCTTTGCTGCTCAGAGGCCCTCAGATGGATACGCAGCAACTTCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG[A/G]AGGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98 C T ---			GGCAGGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAATGCCACT GAACTGTTCAATTAATAATGGTAATTTTCATGTTATGTGATTTTCCACTCAATTAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAATTGCTTCCACTGCCCAACCAAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTTGGAGGTTGCATGACAGGATTAGTCTCTCTGTTT[C]CTTGGT GCAAGTTTGAACCAGTGATTATGTACCATTTGCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTT/CIGGAATCAATGTCTTTTAAATTTTACAGATAAAGAAATTT NCAITTTGAGGAGACATACAAATTTGTAA
WI-20561a	25 A G ---	---	CGTTGCTTATTTAAGATGGCTGTTT/A/GTTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTAA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTACAGATAAAGAAATTT NCAITTTGAGGAGACATACAAATTTGTAA
WI-20116e	69 T A ---	---	GCTTTCATTTTCTGCACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/A/JATAAATCTATATCATATATTTATACACACAACACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATAATGNGCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---	---	GCTTTCATTTTCTGCACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTT/A/JTAGAA CATATATAAATCTATATCATATATTTATACACACAACACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATAATGNGCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---	---	GCTTTCATTTTCTGCACCCAC/C/GTCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAACACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATAATGNGCACAGGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	AAAGATTGCAGTCTGGGACACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAACACAG NTCCCAATGGTGAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGCI G/A/JGTGAACATAATGTTTAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	CTGGGCAGCAAGTAACCAATTTTAAAGAAATACTCTCAAC/A/GJAGTTCTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACTAATTTCTTTGTATTTTATTCGAGGAAGAAGAACTCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCAATTTTGTAGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGAT/CJGCCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---	---	GGCGTGTATTTGATGCAATGTCCAACCAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAAGCATATTACCTCCCCCTTAAGTGACTCATAATTTTC ATTACTTGTGCTAGCTTTTAAAGGTTTAAATAATGTGTAGCATTAAGTGGTATTACTTGAGGGCA ACA/G/AJAATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---	---	CAACTGCTCTGAGGTCTTTCACTAGCTGATTTATAATCCTATATT[AT]AAAAAAATCTATAGTCTG CAGTCTTTTGACATACTTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGGTT TTGTTTGTCTTTTGTAGCTTAACCTGCTGTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTAAATTGCTG
WI- 21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGAC TCTGCCCGCGTGTGCTGCTTCAACTCCAGTCTGTCATGCCCTGTGTAGTGGGTGCCCCAG GTCTGGGCTTCTGAGGTCTT/CJGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCCTC CAAATGATCTAGAGCTCATCCTTGGCGTACATGAGGGGCAGTTGTTCTAGTACCCATTAGCCCC ATGGCTCTTCAAGCCAATTCACACTGGGAAACACACCCCTCAAGATGCCTATCCATTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTA[AVC]AATTATCTA
WI- 21449b	222 C T ---	---	AACAGCAGCAGTCACCTCCAAATGCAAAATAAATTACAAATTTTAGAATAAAATTAATATGTTTA TAATGCGGGTCAGAAAGANTTGAAGGTACAACAGAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCCACTGTGTCAGGGGTCCAAAGCTGACAAGAAAGTCCCAACCTGAGAGGTCTCCACACCC AATCATACCCCTCAGCTTCCCA[C/T]TGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGTGGAAACCGACTCCAGCCTGGAAACCTGCCCTC CCATCCCCCTTAGCGCCTTCTTGCCCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGTCAAGGCTTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAACCCAAACCAAAACAAACAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGTAATGGTG[G/A]AAATTTTCATGAAAATTTCC CCTAAACCATAACAAAACCTGTCTCTTACCCCAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAACCCAAACCAAAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGTAATGGTGGAAATTTTCATGAAAATTTCC CCTAAACCATAACAAAACCTGTCTCTTACCCCAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAAACGTGCAGTCCGTTCAAGCTGTAA AACAGCCCCAAACCCCAAGACATCACAGAGGGCAAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG[G/A]JAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAA[C/][GTGCAGTCCGTTTCAAGCTGT AAAAACAAGCCCAACCCAAAGACATCACAAAGAGGCAAGCAGTGGCAGTGAGAGGAGCCCTGT AAGGATGTTTCAAAGGAGGTCCTCCGCTATGTGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGAAAGTGCGAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---			ACATTCCGAGCCAGTTTTCATATTGCTCCACTGCCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTG[T/G]JACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGTCCTAAGGGCAGGCTACACTTGACTGCA
WI- 21028b	139 A G ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCAAAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGG TTTC[A/G]JTGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCAAAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG[A/C]JATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]JTTTCA TCATACAAAGACAAAGCACAAAGCACACCACCTGCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTTCA TCATACAAAGACAAAGCACAAAGCACACCACCTGCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---			AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAGAAACCTCAAGCTGTGAGGTCAATTTGTAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGGAAC AGATGTTAACAAAAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---			CTCTGAACCTAAAGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTAT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCTTAGGT
WI- 22130b	165 C T ---			TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCCTCCCTCTCCTGACAC CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCATCCAAATGATTACTAGCACTAGGAA GCCAACGGGAANAGGACCCCGCGCTTGCT[C/][GTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

WI-21661	117	G C ---	---	GCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAA[A/G]CTTTAGTCACAGTCAACAAAACTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25	T C ---	---	TCAGTTTAAACACATTCAAGGA[T/C]JAGATTAAATTAATGTCAGGTGAGCATAAAGGGAGATTATAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTATTTCATGGGTGAAGCCCTGGGATAAAG
WI-21636	71	A G ---	---	TGCTTGATTAAATGTGGTGTACATTATCCTATTTACAGATGGAAACAGAAATACCAGCTTTTTTAA[A/G]TAGCAATATCTATTATTATAATAATAATTGAATAAACACCATAATAATCACTAAAGGAAGTAATCTAATTGTGTTGATTTTGCAGAGGGAGAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G A ---	---	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTATTAGACAAAGTAAACATACCTGGACACGGTTTCAGGCATGAAGGATACA[A/G]CAGTTAATTAACTAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCCACTGAACCTCACCCAGCTGAAACACTGAAGGATACCTGGGTAAAGGA
WI-21524b	97	C T ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCCTCAAGTTACTTCTCCAGGGGATG
WI-21524a	35	A C ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCCTCAAGTTACTTCTCCAGGGGATG
WI-22652a	32	G T ---	---	TTACCTTCCAAACCAGGCCACTTTGGAGAAAG[G/T]AAGAGAATGCTATTAAATCAATAAGCCAAAGACAATAGGGACTACCTGGGTAGACCAAGATGGCAGTGCCAGTCACCATCATCTCCGACAGAACCTTTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCCTTAGGG
WI-21703d	197	A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGTGGTGGTGGCAGGGCTCTGTCATCCCCCTTTCCTCAGCACAGCACCATCTTCACCCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG

WI-21703c	134	A G ---			CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCAGCACAGCACCATTCTCACCTCTCTGGAAAGCAGCATTTGGAGCCTACACQ A/GJCTTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGCAGAGCACAGCTAGGGCAAGGACTTAAGGAACTTGTGGGGAAGAG
WI-22663c	139	G A ---			CCCTTGTCAGTCTGTCCTCGGCTTCTCACTGCACTGGCGAGGTGAGCCGGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAATCCGTGTTGAATGTGGGT
WI-22663b	55	C T ---			CCCTTGTCAGTCTGTCCTCGGCTTCTCACTGCACTGGCGAGGTGAGCCGGCTC/TJGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCCTGAATCCGTGTTGAATGTGGGT
WI-22663a	38	C T ---			CCCTTGTCAGTCTGTCCTCGGCTTCTCACTGCACTGG/C/TJGAGGTGAGCCGGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A G ---			TCCTTTATCCTGCTGCTGCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGAGCCCTTGGGATT CCAACTAACAAATTAGTTTCTGTAAATATT/A/GJTTCTAGTCCATTAGATTGTGTAATGATCTAA ATGGNGTAACCAATTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI-22631a	52	T C ---			AAGATATAGTGGCAGGACAGATTGGTCACGAATCCTGGCTTCAGTTCGTGA/T/CJAGCACCATT CAAGTTTAGGCAAGGTAATTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTT
WI-20258	157	G T ---			AATCCACATTTACGAGGGGGACCGCTGCCATGTCGCCAGGCTCACAGCAGCGGGCTAC TCTGCTGGTGGTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCCGTAAGGCATGACAAACG GGAGGCCCGCGGGGTTCAG/GTJCGCGTTGACGCAGGTGCAATGGCTGGCAGCGGCCCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC
WI-22714	212	C A ---			ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCCTACTCTCCTGCTACTGACAGGAGTGTGTGGGAAACGAAAGT CTGAAAAGGATTCAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/C/JTGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G A ---			TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGGCC/TG/JTCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTCGAAGCCATAGTTTGGATGGCAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCAAGGGCCTGAGGGAGAAATGAATTTGGGCTTGTCTACAGGGTGAAGGGCGCGCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAAGTAAAGCTTAAAGCTTAAAGGTAAAGCTTAAAGGT TGGGATATGTTGGGAAT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAAGCTAAATGAGGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCTGCTGCT
WI-22775a	60	A G ---				TGCTGTTTCTTATGTTTATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTACATCAGJTAGTA GGAAAGGGGAAATAAATCCCTAAGGGCAGCAATAATTTCTGTCTTTGAATCCTTCATTGAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGTAAGTGGTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATGAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAAACCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCTCTGCTGTGAGCCCTCATCCCAACCCCTCCAGCCCTCATGCCACACACCCGTGCCACATT CCCCATCCTCCCTGTCTGCTCCCACTCAAGTCCAATCCAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGGCTGTGGGTC CTG/AITGGCGTGGTGTGATGTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCCATTGTGCTCCAAGGTGGCACA TCTTCATCTTTGTTATATATCTGAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTTTGAAGCTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTTCATTTGATTTTTTATTTGTTTCTTCCATTTCTCTGTCAAACTTTTC[A/T]TTTTGTTTATAA ACTGTTTCTAAACTTCACCTAATCTCTATCTGTATTCTTCTGTTAGTCCCTGAACCTCTTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCCAAGAGCTTCT GATTCAGTAGGCCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTGGAAGACCTTCTAAGTGTGCAG ATGCTGCTTGTCCCGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTCTTTTAAA GGAGAGACAGGAATTCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAGCAGAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACCC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGTCTCTCAA AGTATGGCTTCAGACAAGCCCCATTGTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGTGAGACCAAGCAACCTGT

WI-21190	39	T C ---	---	TTTTCCCATACCAATGCACCTGTTTGTATAAACTATT/CJGTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATATTATTAACAAATAATTATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAAGTATGTTTATTTCCATGTATAAAAGCTT AACACA
WI-19937d	186	G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185	C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227	C T ---	---	GAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACTGAAAATCTGTTCAAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAAATACATTTCTGGGG TCCAATCACATACTTCAGGTTACAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATT[C/J]TCTACTGAATCTTGGTGGGAG
WI-21122a	42	C T ---	---	TCACTTTGTATCATAATCCCTGTAAAGCTAAAGTTATTCA[C/J]TTAACAGGAACTCTGTTTTTCC TTATTCAAATGTACAAAGCCTGACGGTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGCCTATTGTGGTTGCT
WI-21254	53	A G ---	---	CAGTTTGTACAGGAAGGGCCCATGAATGTGGCGGAACCTATTCACAGGAG[G/J]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G T ---	---	AAGGAACTGCATGGGTACAAAT[G/J]TCCAAATTCATACTTAACAAGGTGGGAAACGGGTCATTCT TGCCCTGCTCCAGAACAAAGGGCGAGTCTATGCACCTCTG
WI-21059b	181	T C ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATT[C/J]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT
WI-21059a	63	C T ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTTCCCACTGAGCCTGG[C/J]TT GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT

WI-21627b	153	A G ---	---	---	GCATGAAAGAACTCCAATCAGACTTTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATATTAACCCATATTTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI-21627a	106	A G ---	---	---	GCATGAAAGAACTCCAATCAGACTTTTATTCAATAAGCAGCTTTTCAATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAACCCATATTTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI-21399a	75	C T ---	---	---	GGATTTGAGTCCCACTTGATCTCAAAATTCACCTTCTTGCAATGTAACAAGCTCATTCCTCTAAAGTT TCAGTTT[C/T]TTCACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTTCTGCATTTGTCTGAGGTTGTGTGCCCTAGGACTAGGTAGGATCTCTCTTGTCTTCTGCC TTACCTAGGCATAGTGCCCTGATAGCAGGCTGAAGCCCAATTCATACTTGT
WI-20329a	68	G A ---	---	---	CGATGCTCTGCTAAGATAGGAGGTTAAATTCCTTACATGGTGGTCACAGACAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGCTGCTTCTTAAAAACAGTAACCAATCAAAAAGAAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAGGGAAAGGCCTCACT
WI-21249	155	T C ---	---	---	TTCTGGCATTCAAATGTACATGTAAATCCAAATTTAACAGATCAAAATTTGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTTGTATCTAAGTTTCACTTTTAAAGAACATTATAAAGTAAAT AAAACTCTAGGTGTATACCTA[T/C]ATGGAACCTAGTTTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAATTATAAAACATTGAGA
WI-21504	147	C T ---	---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATTACAGTGGGGCAGCGCCGTTCCGGCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGGATCGGCCCTTCGGAGCTCT CAGGG
WI-21242	115	G A ---	---	---	CTGCACCAGGAGGACAGCTGCTGGCAGGACTAATAAACCCCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACGGCGGAGGGGAGGGGAGAGAAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181	A G ---	---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACGTGCGTCTTTGGAGAAAGGCA[A/G]AAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCGTTCTCCACCCTATTTCTCCCTGAAG

WI- 21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGCTCCAAACCCAGGCTTCTC[A/T]CTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGCAGTGGCTTTGGAGAAAGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTTCCCGTTCTCCACCCTATTTCCTCCCTGAAG
WI- 20893d	207 A G ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTCACGTAAAGTTTCATCACCAGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCCTCTCTTTTACAATGCAGT TTC[A/G]ACATAACATTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 20893c	179 T C ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTCACGTAAAGTTTCATCACCAGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCAT[C/T]TTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCCAGATAGGACTAACTGGAGGGTGAAGGAACAAGGTGAAA GGTAT[C/G]GGTCTGGTGAGACAAAAGCAGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTATTCCAGTGCATGTCCTTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAAAGCAAAAGCG
WI- 21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAAATGTA[C/A]AATTAAATTTATTATTGAATTTAGTTACCCC ATTGTGCTATCAATAATTCAATCTTATTCATCTTTGTAACCTATTATTGTA
WI- 21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTTGATACAGATACACAATGTG /A]TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTACAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAATAATTCAATCTTATTCATCTTTGTAACCTATTATTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTGCTGCTCTGGAGGCAACGTCCAGGTCCGGGAAAGGCACCTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCGCCCCACAGGCAGCCTCGGGGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGCTGCGTGGTGGGTCGCCAACAGCTCCTTCTTTGGGG
WI- 21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCTCTAAGGCAGGACAAAAGCAACTTTCCATT ATTCCTAGTTTAGACCAGAAATCTTTAATTTTATATTTCTCTTTAATAACTGTCAAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGTGA[G/A]JAGTAG TATTCTCTACATACCACAGTATACAATGATGCCTTCTCTGCAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	TTGAACCTCTGAAGGTGGCTTATGICTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	TTGAACCTCTGAAGGTGGCTTATGICTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCA[A/G]TCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	ATGAAACATGTTGCAGTGGGATGAAT[C/G]TATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTTCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAATTTAACATT[C/A/G]TCTAGTTTCAGTGATTAGT CACAGAANTTAAACATCTGCCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACCTTGGAAAGTACTACACATGGCAATA AGCAGCCTATCTTCTTTACCAACCCAGAAAGTTTCTTGGGCATGTGATGGCCAGACCCCTTTCCAA GGGAATA[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGGAAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCCAAGCAT
WI- 21574a	235 C T ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAATAATTTGATCTAGCAGCAACTTTCACCATANTATTTAACAGACTCAAAGTGATACATAAGCTTG TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCC[T/C]TGTCTGTCAGGTGGGA
WI- 21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACCTCTAACCTTTTCAGGAAGCTTGGGT GTGACCCCACTGCATAAATGGATTTTCACCATANTATTTAACAGACTCAAAGTGATACATAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTTCTCAGC TTGCCTACTGACCACCTTTCTTTCTAATAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---	---	TGCTTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATTATGATCACTGTTCGAATTTTCAGTCACCTAAATAACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCATGGTATTTTGGGCAGTTGGCTGIGTIGGG
WI- 21615b	151 C T ---	---	GACCGAGAAAACCTGCAAGGCATATGATGTTTGTGGAAGTATCATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTCATACATATAAGATAAGGATGGACT CTTTCAGTGAGTATTAT[C/T]JAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATATTGGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---			TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCCTTGAAGAAAAAAAT/AJGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA
				CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTTATTACITTTTACATGTGGACAATCTAGTTGTAGCGGTTTAAAGGTTAAATTTGG
WI-21660	120 C T ---			TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCTTACTGTGTGTACCAAGAGGAGGAGAGCAGCTCACCAAGCCTAACCTGGCC[C/T]TGTCTTTTTCAGGCTTCTCAGGATGCCACAGCACATACTGGGGAACCTGGGATGCAGGGAGAAAGCCAGGGTCTGTCTTCAGGAGGGTCACAGC
WI-19105c	211 C T ---			TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTTGTAGTCTGTAAAGAGGACACTAAGGCACATGGCTGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTGTCTGTAGGTTTCCAGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCCCACAACCTTC[C/T]TCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCCG
WI-19105a	33 T C ---			TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTT[C]GTGGTCCATGTGGTTTGTAGTCTGTAAAGAAAGGACTAAGGCACATGGCTGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTTGCTGTAGGTTTCCAGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCTCCACAACCTTCCTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCCG
WI-21760c	81 C A ---			CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---			CAACCTAGTCACTCTACTGATGCAATGATTTGG[A/G]GGTGTCTTCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---			TCTGCCATATTGTTCCAGCACCACTATTACTGTATTATTCTCTTTGAGGAAACCAGGNATTAAGAAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGTTAAATCCTTTTCCCTTACCAAAAGGA
WI-20934a	72 T G ---			ACTTCTTAATCACCAGAGAAACAGAGGGGAAGACTGAGATATGTTTGCAGAAATTTATCTAC[T/C]AGAGACAATTTCATAGTTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGC
				CCAACATGCAACATAGTCTTTCATTCTTAAAGTACATAGTAAGGTATGAAAAACATTTGTATTCAAGAGAA[T/G]TCTAAGACAAATGTTCAATATTCAATGGCTGGCACTAGTGGTAATTCAGCAGACAAACAGCATGAGAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCCAATCAAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCAGGAGA
WI-21561	55 T G ---			TTTCCATTTTATTACGCCGGCCATCAGAACAAATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAACCTCTCCAGGCAAGAGGAAAGTGCATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTTTTAGAAAGTGCTTATTAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGAATAATTTTGTGTAATCTGTTTAAAGATTTTGTGGATGCATTTGTCCCCCA

WI-21961c	200 T G ---	---	AGCTTTGCTTGAAAAATTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTATTATTATTTT TTCCGTAAGTTATTGGGTACAGGAGGTAATTTGGTTATATAAGTTCTTTAGTGGCGATTTGTGATTT TTGGTGACCCATTACCCAAGGAGTATACACTGCACCATACCTCGGTCTTTTATCCCTCGCCCC[T/G]C TCCACCTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGC
WI-21961b	73 G A ---	---	AGCTTTGCTTGAAAAATTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTATTATTATTT TTCC[G/A]TAAGTTATTGGGTACAGGAGGTAATTTGGTTATATAAGTTCTTTAGTGGCGATTTGTG ATTTGGTGACCCATTACCCAAGGAGTATACACTGCACCATACCTCGGTCTTTTATCCCTCGCCCCCTC TCCACCTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGC
WI-21956	26 T G ---	---	CCCACCTGGGTCCTTTCAAGTGAAT[T/G]TTCCCTTCGTTCCCTGTTCTAAAGCCTTTAAATGAAC TCCATTCCCTGTTCTGAACCTTGCCCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTTCTT CTGAGCGGCAAGGACTGAAGTTGCTGTGACCTGTAGGGTTCGACCGGTAACTCAGGGTAACCTC CTATCTCTCCACCGGTAAACAGAGGGGTACATTATGGGGTCCAGGT
WI-21966	148 G A ---	---	CAACATACATTATGGCTGCCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATAT TTTTGTTAGAGCATGAGTGAGAGTGTTGTGTGTGCGCGCGCGGCGCATGGCAGTGGCAGG GGATTGCAATGGG[G/A]AACAGGATAAAAGGTATAAAACCTTGGTCCGAAATCTTTGCTTTATTAAAC CTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGATCCCATCA CCTGAGTAGTGATACATTGTACCCAACTTGAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCAT TTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTTCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	GCCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCA CTTACTAAGTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTTCTCTGTGAAATGGGTACAA TGTTGGTCAAGCAGTAAGGAACTAATACA[T/C]GTACAGCACTTCAGCACAAAGCCCTGGGCACACAG CACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGGACAAATTTTAAAGTACGTGGCCAGC TGTTGGTTGCTCTTGTTGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAAGTGTAGTGGTTACA AATTTGTTCTCTTCAGTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAA[G/T]TATTAAATTAATTGCATAATTTGAGGGCTACTCT
WI-20317b	217 G T ---	---	CAGGACTTGGTTGCTGTCCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATTGGTTGTGCG TTTTCCTTTTTGATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGTCTTATCCGGATGACGGAGG GTACACGGGGCTCCGCTCAGTCCCGCCGAAGGACGTATTC[G/A]CTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCTCTTTGCTGCAACCTCT
WI-22082e	179 G A ---	---	

WI-22082b	67 C T ---	---	CAGGACTTGTTGCTGTCCTCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATTGGTTGTGTG[C /T]GTTTCCCTTTTGATAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCGTCCGCTCAGTTCGCCGCGAAGGACGTATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAATCCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ---	---	AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAAAATTTACAGCAAT TAAACAGTGTAGTTTGTACAATAACACATATAGCAATGATACAAATTAGGGGAAACCCCTGG GCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGGCCTATTTTCAGGCTTTCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	AAGCGATTTTATTAAATTGATTGGACATACTGTAGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	AAGCGATTTTATTAAATTGATTGGACATACTGTAGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---	---	CAACAGATGCTTGAGCCAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTTT[G/C]CCCCATTCTTCTAATCTCTTTTGCCCTTACAA TATAATACCTTCTAGGTATCACTCATCCTATAGGAATGCCCTTCTAGTTAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	TGACAGATCACACCACATTTTGTGTTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAGAACAACATACACACATGTGCACACACI[A/G]AGAGGGCAAGTACAAAAATGTAACC CCACCAAAGTGCAATGAATGAAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCTAGGCT
WI-21761b	138 C G ---	---	CTGAGGCCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGAAATAACTGAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTTACATCTTCTCTGCGAGTTAAACGTGCCGTGG CT[C/G]CAATACACACCAAGCCAAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCAGTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGTAGTGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGTAATAGGCATGGGCAAT

WI-21079a	50	G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG[A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTTGATTCTCCTCATGAATTAAGCTGTGTGCTCACTTGTTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGAAATTTACAACCCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45	T G ---	---	TCTGTAGATTTTAGCCATGCCATATATTTAACTTTTAAGGAAAG[T/G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAATATATAAATAATTTGGTTGCAAAATTCAGNAAGGGCA TTAACCAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A G ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCTCCCAAGAGGACTCGGAAGATGTTGATTCCAGGGCAGAGT GAGGGGCAGAC[A/G]GGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCTCACCCAGAGAGGCTCACTGCTGACCTGACCCACACCCACTCACCC CAGCACAGGCACACGAGGGCACACGACACACGNTGCACTCACACGC
WI-18916b	42	C T ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-18916a	35	G C ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-19828c	200	A G ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAACAA GATCAGAGGTGCTAAGTGTGTAGCTAGTGCAGGCTTCTGGCCCCAAATCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTACTTCTTCTGACCTCACCACCCCAAAAT[A/G] JCTTTTAATTCTGGAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T ---	---	CACAAAGTCTGTACAACTTAGGGACACAGCCCTGGCCCTGCCCCTC/TJAGCTGCATGCCACCCCTC ATATCCCACCCCATCCCCAGCTCCTGCCCCGACACCCCAAGGCTCCTGCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCCTTGATCCAACACAGCATCT
WI-19860	51	C G ---	---	TTGACCTAAAGCCTAGCATAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTTGTATTTGCCATTACCCCATAAATGGTGGGATCTACCTCCCCCT CCTTGCAAAATTTGAGCTGGNCCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80	C T ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCATTTATTTCCCTCTTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACCTATTGC

WI-19891c	172 C G ---	---	TGTTGGTCTGAGAAATTCACAGCTTACTACAAAGGAGCTGAGAAATGCTTGGTGCCCTCCCTCCCTCCCGG ACTCCTCTGTCTCTGGGAAACGTGGCTTGNCTCCAGACACAGTGTGATGCCAGCTCTCTCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC[G/G]CGTCTTCCCGGGCGTGGGGCGTGTGT CAGGCAGGCGGGGAGGAGGAAAGGAGGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTAGCTTCCATGTTCTCCAAGCACGGGCTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGG[C/T]GCAAAACTGCTTTGAGGAAATNTCCCGAGGAGGAATAAACTAGAACGCG ACCTGCTATTTACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTTCTGTCCAGTCCAGAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAGAACAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA[T/G]ACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGTGATCTTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGTGGGAA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAGAACAAGCAGCTGTACAGGAGTGGGACGCG[G/A]TCAGTGTAC AATACATTGATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGTGATCTTGTTTCCCGCAGAGGGCTGGGAGGCGGNGGGTGTGGGAA
WI-20622	130 T C ---	---	CCACTTCAATATTTACAAAATGCTCACGCGCAAAATATGAAAAGCTTCAACACTTCCCTTTGTA ACTTGTGCAATAAATGCAACTTAAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACATTTTAAATGACATCATTTGCCAATACATA CATTATTTCTNTAACITTTATTTTACAATAAGCCAACATCTGTCATGCAG
WI-20768b	190 C T ---	---	TTCCCACTCAAACTCCCAACCTTCTGGAAGGCGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATCTGTATATCACCACTCTA CAGGAGAGGTCTATTTCTGGGCACCCAGAAAGNTCAGCACACATACTGCTGGG[C/T]CAGGGACTC GTAATTCGCCCTTGGTCCAACTCCTTCTATGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TTCCCACTCAAACTCCCAACCTTCTGGAAGGCGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAAAGNTCAGCACACATACTGCTGGGACCCAGGGACTC GTAATTCGCCCTTGGTCCAACTCCTTCTATGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGCCTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTCATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTGTTGGTCATCTTTAAAGAAA TGTCTTAACATACCAAG[A/T]JAGTGGAAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACCTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---				TGTTGCTTTGGTTGTTGCTTTCTGGAAACATATTGGAACACTTGTTTTCATATAAGCTGCTCCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCAATTATGAAATCTGAATTTCTT[A/G]TTAAT ACTCTGGTGCAATTCATTCATCTGCAAAAGCAACTGGCACAACCACTCCTTGCCGGTGCACTCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---				CCAAGGATGAAATTTCCACATTTATTTTNCCTTTTATGTGAATAGAAAATGGCAGTGAAGTGCTCCTATG AA[C/T]GAGGCGAGGAATGGGCATGGCGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---				GGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTG[C/T]TCATTTGCAAAATAAAACCCA GACCGGTCATCTTTTCAGTTCCCTTCCAGCTCTATTATTTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---				GACGTCACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCCTCTAAGCAOCCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGGACCTTGCTTTT [C/T]TTCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCCAAATGTGCTAAGGTCCCAATCCAGACCCCTCCAG
WI-22292	53 A G ---				CCAGTGGAAAGGTTTACAGCCATAGTGAGTTCCCCCATTTGCTCAGTACCAGA[A/G]GTTTGAGTAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---				ACCTTGACACCTGCCATCCGGTGCCATCTCTGCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCACCAAAATGGGCAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGTCTAGCATCCAGCCTCTCTCTCAGCAAAAGGCAAGGATTGTGG[C/T]CCTTGTTTCTG AACAGGCCCCAGGGCAGCCAAAGGCATGCCATCACTGCAGCACTCAACCCT
WI-22395b	127 A G ---				GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTCTTGAATATTTT GTAGGGATGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAAT[A/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---				TTTATGGCTCCTGAGTGCCCTTACCCAGCTACACTTTACCTTGATCTATATAAAGTGTAATTTAGAGT AAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---				CCCTTCTGGACAGTTTGCTTTATGTGTTTCAGACAATCAAGGNTCGCCTTCCAGGCACAGCCAGTGCTT [C]CTGGATGGCATCAGCACAGGCTCCCTGCCCGCCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---				ATTTTCCCTTTCTGTGTTTCGTAATTTCCCTTTTGTGTCAGTAATNAGCAATACACTGA[T/C]TGGAA ATCTGCATGATTAAATAACATTAAACAAGTTTCATAAACACACCCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTGCACATTCTCCTCTAGTT T

UTR-04932-2a	149	C T ---			GCAGCCATCCTCCTCCAAACACCTCCAGGCCACCCCTGGGCCAGAGCACCTCATGCCAGCAGCACCTACGTTGGCCCGAGTACGGACCCGCTGGCCCGCAGGTTCTCGGCTCTCAGACGTCOCAGCAAGTGGA
				---	GCCCAGAGGTTTG/C/TTTGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTTC
					TTTGACGGGGCCGCTGCTCAGCTGCTCCTGGAGGTGAGGAAGAGGT
stFIBBb	412	G C ---		---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTTCCCAACGGCCCTTGCCACTGCTCTCTGGCCCTCTCTCTGATCATGCCAGG
					TTTGCAACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA
					AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C ---		---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTTCCCAACGGCCCTTGCCACTGCTCTCTGGCCCTCTCTCTGATCATGCCAGG
					TTTGCAACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA
				---	AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
					GTCCACAAGAGGCGAGCGCTCTCGGAGCGTCTCCACCATGGCCCTGGGCTCTGCTCCTCAC/T/C]CTC
stGLV2	61	T C ---		---	CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGCTCTCCTGCTCAGGCTACCGGGGCCAGCACTGACTGCACTGGCATGT
stSG1001	70	T C ---		---	GTTCAGGCTCATCTTGAACCTCCTGGTGTCAAGCGATCCTCCACCTCGACCTCCAGGGTGTGGGAT
7c				---	TA/T/C]AGGCATGAGCCCCCACACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT
					TTAAGAGAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001	33	G A ---		---	GTTCAGGCTCATCTTGAACCTCCTGGTGTCAAGC/G/A]ATCCTCCACCTCGACCTCCAGGGTGTGG
7a				---	GATTATAGGCATGAGCCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT
					TTAAGAGAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002	63	A T ---		---	TAATGATAATTAGGGCATTCTTCCACACGAAGATGACACAATTGACCCAATATCATTGAGGC[A/T]
3				---	AACAGTTTGGGCTGTTTTCAGTAGTATGACAGTGA
stSG1009	36	G C ---		---	GTGGAGAAAGATCGTCTTTCCTCCCTCCCATGACC/G/C]GGCTTCCCGGGCACCTGTGCGTTTTC
6					ACCCCGAGACGGCCTTGTAGGGACCCACTGCCCACTCCGCTGCTGTGCGTGGTTCGGCCTCCTAG
					GGCTCGAGTGTTAAG
stSG1011	107	C A ---		---	TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCTGAGGGCAGTACCCCTCATTGGGC
8				---	ACAGTCCAGACCCAAAGTCAAAGATGCCCATTCCTTGGC/G/C]CTCAGCCCTCAGTTCCCTTCATTTC
					ACCAGGCCGTGCCCTGTTGAGTTTTTCTCCAGTGAG
stSG1012	89	T C ---		---	TAGTAGGTAAGAAAAGCAAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTGAGACTATGC
0				---	CGTGTTACGAACACITTAATA/J/C]GTTGTGTAACTGATTTATCCTCGTCTTACAAATG
stSG1017	42	C T ---		---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG/C/T]GGGAGGAGAAAGTGAACAGGAA
8					TCGATTCTTGTCTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC

stSG1019 3	136 G A ---	---	GGAACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC TIG/AJTTTGAAAACCTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 G T ---	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCCCTGGCTTGGGAG AGTCAGCCTTGGTCACCTCATAACGGGGCTCCAAGCTAAGGCGTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA[G/T]CAAGACCACAAAGGCAGATGCCCACTGCTGCTCTTCTTCTGCTACTTTCT
stSG1020 9b	75 A G ---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATTCAATAAACTAATTCTCCTTAAGATCCCACTTTAT TTTTTA[A/G]CTCCAATAAATGTAAATTATCAGCTGCTGAATT
stSG1020 9a	34 C T ---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCTCCTTAAGATCCCACT TTATTTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 T C ---	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 A C ---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAAAAATGAGAAGATTCTTTTATTTTGGACCAATTTT AGGCACCTTAAGAGTTTCTTTCTTCTTCCCTTGATCA[A/C]AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915 0	123 A C ---	---	CTGTATTAATTAAGAGGCACTATTAAATGAGGACGGAAAAATCTACCTGTACACAAAATCTGTAC TTTAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG[A/C]ATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 T A ---	---	TTTTTGTAAACCAACCCTGAAAGTTTCCACATGTGAATATAGATACAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAAAAAAATAGTACATGTTA[T/A]GTGAATAAAATTAATTTACAAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGAGGAGTAATCCTGG
EST14096 8	71 G C ---	---	GGGATGTATATTACAGATAACACAACCTCACAAATATACCATCAGACATTGAAAACCTAAGGCCATTCT GTGA[G/C]JTATTTTAAACTTGGTGTTTTGCACATAATGATCTTAAAAAAATGAATTAACCAA ACCAAGATTCTCTTCTAAATGAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 C A ---	---	TGCAAAATTGTGAGAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTCG CAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA[C/A]CCCTTC TCTCAGGGTGTGGAG
EST22555 7	60 G A ---	---	TCAAGCATGTGTAAAGGCACCTGCCCGCCAGACCCCTTCTAATCTTGCACACTGGAAGGT[G/A]AAA CCTGGGAGAGAGAACACTCCCTCCCTAGCTTCTACCTGGGCACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---			GTAAACCTTGCAAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/T]TGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---			CAAGTTAGAACCATGTCATCAGCTTTTCATCCATGGTGTAACCTTAAACCCTCAGGCTGCTCTACTCA[V GTGTGGTTTGCTAGCCTCAGCTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACTCTCCA
EST36745 3	56 A G ---			GAGGGGAACTTCAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAAAGTC[A/G]CTATGG GGCCAGACTGAGGTTGGACCCACACAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
STS- R37410c	201 A T ---			TGTGACCATACCAAACCTATGCAATAAAAGAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACACATTTATAAACATTTCTGGTATG T[A/T]TTATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410b	139 G T ---			TGTGACCATACCAAACCTATGCAATAAAAGAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTAT[G/T]GTTTGAATAAATAACAAAATGTGTGATCTCCTGAGACACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410a	48 C T ---			TGTGACCATACCAAACCTATGCAATAAAAGAAAGAAAAAATCCTCA[C/T]TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAATAACAAAATGTGTGATCTCCTGAGACACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R42778	74 C T ---			TATCGTGGGAAGTTCCAAACCTCATACTTATGCTGCTTTTCTACTTGTCTAATAATTGGATGCTTCTTGCCA GGCTC[C/T]TTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCCCTGAA
UTR- 04350	125 C G ---			CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGATGGTGAAATGTTCGGGACCTAGATA[C/G]TGACGGA AGTAGCACGACACTGTGAGTGCACTAA
stSG1026 6	55 T C ---			GAAATAAACTAAACTGCAAGCAAACTCACTGTTAATAAGAAATTGTTCTTCTGT[T/C]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCCTCAGAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1028 2	70 T G ---			GTATAATTCAGCATAAGCCAAAGCCTTTTTAAATAACCAATACTATCATTTTATGAAATCTTTACA AGA[T/G]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A ---			CACCTTAGATATGAGGAAATGGTTTTAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAATAACAGCAATAATTTTTCACCT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCCCAGAAAATGAGAAAAGGATAACAACTTTTGATAAAAAAGGTA AGAATTTCTGTGTG

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGATTGAAATAAAGGAAGGATGCATTTCCGG GCTCCAACCTGCTCCTAGGAAGGCTAGACCTCAACACCACTCCAT[C]GCATTTCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGATTGAAATAAAGGAAGGATGCATTTCCGG GCTCCAACCTGCTCCTAGGAAGGCTAGACCTCAACACCAAT[C]CACCTCCATGCTCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---	---	ATTGGCAAATGGGAAATGACACCAATCATTTGATTACAGAAAATGTTTTATAATCCTCCTCTTG AAATTATGTTTCCAGGCCAGCATGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTT[C]G/AJAAAGTATTTCAGACCAAAGGAGGT
stSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCTATAAATTTGAACATGTTTCTTAC[G]ACGCT TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCTATAAATTTGAACATGTTTCTTAC[G]ACGCT TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1385 b	117 T G ---	---	TTAATGTATCCAGGGAGGGGCCAGGGATGGAGGGGAGGGTTGAGGAGCGAGAGGCAATTTT TGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT[C]TCAATCATTAAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCTGTCG
stSG139	69 T C ---	---	TCGTCTCCTTCCAGTCTTCTGCCAGAAGCATCCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT T[C]GCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATTGTGTACTGTCTGTGCTGCC
stSG1427	103 T C ---	---	GATCTGGTTCCAGACAAGGCTGATTCCAGAGACTCCACGTTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTCA[C]GAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAATCCAGCAGCAAGAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1471	50 A G ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTTAGGTCC[A/G]CTCCCTTGCATGA AATGTGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1483	44 T C ---	---	CAAAACCAAAATCCTTCCACGATATAATTACTATTAGTCTAAG[C]TTTAAATCAAGGTTGAGA ATGACGAATTCAGAAATTTCTTTCATACATAAATTGCTTCTTAGTCTGCAGATGGTA
stSG1696	67 C G ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA [C]GJAATGTGGAGGATGTCTGTTCAGCTGTAGTTACTAATGCAGGAAACCAATGCAAGAGGAA AATGCTGA

stSG1847 b	95 G A ---			TTGCAGACAACATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAACAAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCAAATGTGAAACCAAATTAATAAATAACTTGATCACTGTGCT TCAACACAACTG
stSG1847 a	49 C A ---			TTGCAGACAACATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAACAAAGTGAGAGACC[GTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTTCCAATGTGAAACCAAATTAATAAATAACTTGATCACTGTGC TTCAACACAACTG
stSG1897 a	83 A G ---			CTTAATGCCCTTCCTCTCCTCTGACAGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[A/G]GCCCAACCACCTTCTCCTCCCGTCTCCCAAGATGACT
stSG2022 a	86 T C ---			TGCTCTGAGGTTTCAAACTCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTTAACATTAAATATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTTGT TGTTATTTTTTCTCCCTACAATAATTTCTGACTCTGTAGGACAGTGGCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---			AAACGTTGTCCCAAAATTGTGTTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACACTTAAGAATATATTTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 A G ---			TTGAGCAAAACAAATGATTGCGGAATTGGGAGCTCCAACCAAAATGATTGAGGGGCTCCACAGAGA GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---			TTGAGCAAAACAAATGATTGCGGAATTGGGAGCTCCAACCAAAATGATT[C/G]AGGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTTATTTTAAACAAATGACTGCGGTGTA TGAATCTGACTGTGTGAATAATCTCAGAAATGGCAGCACCACTGGCATGGCGATGGTGAGGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGCTCTG
stSG2141 a	113 C T ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTTATTTTAAACAAATGACTGCGGTGTA TGAATCTGACTGTGTGAATAATCTCAGAAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGAGGTG GGTGAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGCTCTG

stSG2148	50	A G ---				TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTGTAGACCGTGATTTC[G]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---				CTCAATGAGGACTCCATCAGCCAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGAGTGGAAGGACCA
stSG2189	41	C T ---				CAAGTGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACCTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGGGAAC
stSG2200	49	T C ---				TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTATGTAT AATGTCTTACCTGATGATACCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---				CATTTCTGCTCTGCTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A C ---				TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGCGAGGCTATCAGAAGGGCAG[A/ C]CTGTCAAGAACTCTGCCAAGCACTGGGCTGCTCCTCAGGCAGAAATTTCTTCCT
stSG2306	67	A G ---				GTCATCAGCGTAGAGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---				GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAA[T/G]TGCAGTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63	T C ---				AGAGCAGAAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGCAC[T/C] GTTCTCAGAGTCACCAATTACGGTGACTGTGTCTATTCTGGCTGTGCTTCCTATTTCATCA
stSG2465	76	C T ---				CAAGACTAAGAAGCCGCAACCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140	T C ---				TTGCAGGCTTGTAATCCACAATAACAAAGTCATGTATAGAGAAATGTGAAATGATACTTGAAACCAA GATATATAAATAATTGAAGTCATTTATGCCCTTTTGTGACTGGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCAACCCACCCCTTTTAACT
stSG2577	123	T G ---				AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTGCAATCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATC CCGGCCCAGATTAATTAT
b						

stSG2577 a	121 C T ---			AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTCATCCAGTTTGGT CCCAATATAGCCTTCTGCAAGAGAGATCAATGCCGAACCGAACTGTGAAAGC/TATGAACAATC CCGGCCAGATTAATTAT
stSG2700	58 G A ---			ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTAAGACTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGGAAATAAACCCACTGGTCCAGAGCAGAGGAGCTACTTGAAGCCGGACACCA
stSG2724 b	101 T G ---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTCTTTTATATTAATTTGCAATGCTATAAT TTAATACTTATATCCCAATTGCTTGCATAATCA/T/GTTTTTTTAAATCCTGGGTGTGAAAGAAC
stSG2776 a	65 G A ---			GTGGCCGATCTTTACTTTCCAGAAAGCGGTAATAAATAAACCTGTAGAAAGTCTCGAATATGC/G/ AJTATTGGCCCTTTGGAGTTAGGCCAGGAACTTCAACAAGGGACACTGCTGGCCAACCCACAAA ATATCCACTAATTCGCCAATATAGTAACCTGCTTGTCCGAATG
stSG2791 b	109 G T ---			AAGGAAAGGTGGAGGGAAGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTATACTTCTGAACGGTAAGTAAGCAATTTTAAATAATTT[G/T]GGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100 A G ---			AAGGAAAGGTGGAGGGAAGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTATACTTCTGAACGGTAAGTAAGCAATTTTAAATAATTT[G/T]GGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2826	85 C T ---			CCGCAATTTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAACAAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAATAAAGAAAGAAACCCATGAAATGCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A ---			ATGGGTGCATTGTAAAGGCAATTAATACTTTTTCAGGCAGGGGTGGCAAAATTTAATGAGCTGA TGTTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
stSG3031	71 T C ---			ATACTCACGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCCCTGGCATTTTCTGTGTGTCAGC AAAT/C/GCCCCCTTTATTTTAAATGATTCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A ---			GTCCCAACTCCTCTCTTTAGAGAAAACCTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAAAGCCAAAAGGCAAACTGGCTGAGGC
stSG3092	94 T G ---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTTGTCACTATTGAAAACAAAGCCAAAGTTC CAAATCCAAAATAATAATGAACGTGC/T/G]GATAAACATTCCTTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G ---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAAGTGGAGTC/A/G]GTGGGTGCTAAGTGTCTGAACTGAAGTAG
stSG3245	160 G C ---			ACATCTCATCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTCTACCAACCCCTGCCATCCAGTCTG GCCCAGTACCTACCTGGGAGGTTG/C]TGTACTTGGCTTAAGTACTTCATGCTTTAT

stSG3265	42	T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTATTTATAAGGAA[T/C]GCATTGTGAATAGTTTCTCAG TTTTCAATATGGAAGATGATGATTTAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTAGTACAAATGGAGACAGCTTTTCAGGGCAAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141	C T ---	---	TGTACTTACTGTGTCATCCTATCCATCCCTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]TGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3269 a	24	A G ---	---	TGTACTTACTGTGTCATCCTATCC[A/G]TTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3284	130	C T ---	---	TAACTCAAGAACTTTTCAAGTTACAGGAAGATTTATCTAATATTAATAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTTGTTTGTATCCCC
stSG3292	99	A T ---	---	GTCTCAAGTGAATCTGTAATAACATTTTAAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAAGTGACTTAAATATCTAA[A/T]TACAAATCAAATAGCATTTTCTAACTTCAA
stSG3323	26	C A ---	---	TAAATGTCATATCTTTAGCTCTCACT[C/A]CCAGTGTATCCATTTTCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCGTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTTCAGACACATCCATGCTGTAGCATGCGTCAGTGTTCATTCCTTTTAA
stSG3369	69	C T ---	---	GATCCCAGTATTATTTTCTAAATTGAACCTTGTGTGGAAATAAAAAATCTGAGGACCCTCAGAG GG[C/T]ATAAGGGAACCCCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3398	125	G T ---	---	CAAGACTGTAAAGAACGTAGGCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAGAGGACAAATAATAGAGACT
stSG3416 a	43	A G ---	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173	T A ---	---	GTAAGACAAAGGTTTTGCTATGTTGACCAGGCTGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCGCCGAGCTTTTAACTGAAT GTTGAAAATCATCTGCTCTTTGCTGGGTAACTGAT[A/C]AAGTTGCTTAACCTTTGTGAAACCAC TTTCCCTATCTGTAAACAAATGGACAAACAGAACTTTTCTTCTCTC
stSG3436	88	T A ---	---	GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGCTGATGTGATGGAGGCTCAGAGA ATGAGTGGCAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTCTCTATC

stSG3463	103 C T ---	---	GATACAGAAGATAGTGGTATGGATAGTAGTGAAGGACAAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTAC[C/T]TGGAAACAACTTGCTTGACTATATTA CTGA
stSG3491 b	71 G A ---	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGTGGCAATATTTCTCAGCAACAAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTTATTAACACTCATTTTACTATTTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAAACACACACACC CCTAATTCCTCAAATGCTCTTGGCATAAGTTTATCTTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTTAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGTAGCCTACCTACACAGCTGTACAAAACCAAAATACAGAAATGGCTTC TGTGATACTGGCCTTGTCTGAAACGCATCTCAGTCTATTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAG[A/G]CCCTGCTGGGTCTCTCAGTCTTGCCATGAAGTATG
stSG3583	112 G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCCAACAGGATCTACGAACCTGGCATGATCCA CATCGCTACACATACCATGTCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101 T C ---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCCCTGGCACAACCAACCCCAATGA[T/C]CCTATTCCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTCTTCTAAAAAAA AA[A/T]TTTCTCTGATGCTCTTGACCCCTGTAGGAAACACATTTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTTCAGCTTAAATTTTCTTGAATTCATATACGCT TCTGTCAATT[A/C]AACAAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAACCTGCCATTAGTAGCCATATTTAGGATGAGA[T/C]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAATAATAAGTTATCTGGGAAACGGCCATTTGTCCAACATTTACTAA GIGCCTACTA
stSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAATATATGATGATAACAAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACCTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCCTCTTTGTA
stSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATTAACCTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCCTCTTTGTA
stSG3693 b	85 A C ---			ATTGTTCCCTGAACATTCCTGGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCCACACACGGGAAAAAGG
stSG3693 a	30 C T ---			ATTGTTCCCTGAACATTCCTGGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACACGGGAAAAAGG
stSG3698 b	145 G A ---			TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCCAATCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---			TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCCAATCCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGGTCTCTGCTGGATCCCAACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACCTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGT
stSG3725	104 G A ---			GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACCAGCCAAACAGCAACAGCC[C/G/A]JAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAAATCCACATCATTGTTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---			GACAAAGAGGGAAGAGATGCGCCAGAGACAGGGCTGGGCAGCTGGGGTCCCTGAGTGCCAGGCGC CACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGTCTA[G/C]JGGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT

stSG3880 a	36 GC ---			GACAAGAGGAAGAGATGCGCCAGAGACAGGGCTG[C]GGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGCTAGGGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT
stSG3895	44 A G ---			AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTG[C]GTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTTCGTCAACTG AAAT
stSG3902	104 T C ---			TCTGTTGAGACTGGAGAGACGAGTACCAAGCACCGACTCTGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACACCTAAATGTGAAGTCTTTCTTTCT[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGCCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---			GGGTGCTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[C]G[A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCACAACTTCCTGGACGT
stSG40	25 A G ---			GAGGAAGAGGTTGAAGAAGTCTGA[C]G]AAATATATTTAAGATTTCTTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTAGATAAGGAACAATAAACCTTGTGTATGTATCA CCCA
stSG4009	32 A G ---			GTGTGGGCTGTCTGATGATGAATGGCGGCTC[G]G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATTCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCACACTGCTTACA
stSG4033	123 T C ---			AGAAAGCCTTGGGGACAATGGCAGTGGCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[C]GTTGTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---			GCTGAGAGCACGTGTACAGCCACGCCTGT[G]A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCCCTCAGTCAGGAGGTTCCAGGCTCCCGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---			ACTGTGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAATA[C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAAAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 GT ---			ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGTAGATGTATTAG[C]TATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---			ATCTGGGCTGAATTAGTCAAGCAGGTC[C]G]GATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65 G A ---			TGCATGTTCCACATCTTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[C]G/ AICTTTTCCCTCAGAGAGGCCACAGTTAAACAGGTTCCAGCACACCAATTAATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATAGACTTTTCTTGTGTACATTTCTTGA/GTATATATTTT TACTTCTTCTGAAATGCCACATAATTTGCAATAAATGATTCACCTCCTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTC[G/A]GC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACACAGAGC[G/A]CCACGGCCGGGACTCCCGCATGGCTGGGGG GCTATGGCTCTGACAAAGAGATGAGCGAGGCGGGGCTGCCTCCTCCCCAGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACATTTCCAT TTAAGCAATAAAAT/G]AGCTTCTGAGTAGTTGTTCCAGTTTACCCAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAGGCCAACACACAGAAAAGATACAAATACATTCACAGCTAATATTTAGTTTATGACAC AGAG[T/G]TTTCAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAGTTTAAAGTTATCACTT GGAGAGCAGATTTCTTGGCCTCGCCCTTGATCTGTTGAGGGGTGTC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAAACAAATGTGTACACCTGGAGCTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGC[A/C]CCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAACTCTGCTTTGCAAGTGTCTCTCCAAGGGAG AACAG[A/G]CTGGAACTGCGGCTCTGCAAGAGCCATTCTTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTTCTTT[C]TCAGTCTTGTAGT ATCCACAGTAGTGATGCTGTCCATGTACAAGTGTCTGTCCAGAACACCCCATTAATTCATGCC ACCAATGGTTCTGTATGTGCATCCGATAATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACCCGC[A/G]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG4443	65	C T ---			AGCAGATCAGTCAGCCCACTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430					TGTATGCAATGAGAAATAACCAACTGTAGGATGGGGAGGGGAGGCGAGGGAATAGGCAC
a	54	A G ---			AAATGGAATTCTATCTGGCTGTCTCTCTCAGGTC
stSG4448	99	G A ---			ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGT[AG]ATTAAACATA
					GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
					CCTCCCTTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCTCCCTCCGCCCCACCCAGGCTCT
stSG4449	92	T C ---			CGCTAGCCCTGCCCTCTGGGGTCACTGC[G]ATGGGTTAGGCCCCCAAAAA
					ATTAGCCATTTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
					TAACTTTGGACAACCTTAAACTTA[7/C]TAGTGACATTGCTGTCTAATAATCAAACTACTTCATCATA
stSG4449	92	T C ---			GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
					CAGACATGAGGGATGCCCTGTCTCTCTGGGACAGAGCCCTCA[C]AAGATGATGTCCATGTTTGTGT
stSG4467	42	C A ---			GAATGAAACTCAACACTCTTCAGTTTTTAGAGTCACTTTCTGTTATCGAGCGACACACCGAGGAG
					CACACCTGCTTCCAAAGGCTGCTGCCCTTCTGCACACAGT
stSG4475	21	A C ---			ACATGTCATTTCTGACCAGG[A/C]ATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGGA
					TTAAGAGACACAAACTGGACTTTTGTCTTTTACTGTAGCACCCAGGTTTCATG
					GTAACATTCTGGGGTGGGGTGAGACAAACA[A/G]ATGAACCAATAATTAATTACAATTATACATT
stSG4477	32	A G ---			TCAAGGAGACTTTTAATCTAGGTTAATGTGAACGCAGCCATCAATGTTTGTGTCAGGAAAGGGAGA
					TGAAGTCTTGCTCTGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
					TGAACTCAGAGCTGGTGGGAGCTGCAGGCAAGGAGGCTGGGGCCAGATGAGCCGCCGGGA
stSG4531	79	C T ---			CAGCAGGCGTCG[C/T]GCCACGTCCTGCGTTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCT
stSG4550					GATTCTCATTGACAGGGGAGACGCTGTTGTCATCAA
b	86	G A ---			TGCATTAAGGAATGATACGGCATAATTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
					AAAAGAGACAGTGGGCAC[C/G]CAATTGGAGGGGAAGCGGGGCGAGGTTTTAGAGAAC
stSG4550	85	C G ---			TGCATTAAGGAATGATACGGCATAATTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a					AAAAGAGACAGTGGGCAC[C/G]GCAATTGGAGGGGAAGCGGGGCGAGGTTTTAGAGAAC
					AATCAGGCACAAGCTCGGGAGAGAGCCCAACAAAGCTCTTCTGCAC[A/G]ATGGGAGGGAGACAC
stSG4590	47	A G ---			CATTGAAAAAGGCATCGTTCCTTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
					AATCTGTATCACCCAGCGCTGG[T/C]CAATGTACTAGTACTTCCACAGGGATTTTTTATACTATTC
					CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTTATCT
stSG4623	22	T C ---			TAATATCTCTTCAAGATGCTCTGGAG
					TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTAGTTTTTATGTTTTCAGATTTAAAG
stSG4843	102	A C ---			GTATTTCTCTTAGCTTCTAAATTTTGAGTCA[T/C]ATCAGAAAGTCTTCCCTACTCCCAAGGTGA
					GAAAGGA

stSG4850 a	38 C T ---			GGAACTAAACTGGGAATGCCGAGGAGGAAGGGGCTC/C/TGTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCCCTGTCGGGAGGTTTCCAAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G ---			AACCTCTGAAGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCTGCTTTTGCAGAAATGGCCTG CCCCTGGGACTGGAGCAG[A/G]CTTGGGTGAGCTCTAGGTGGAGGGTGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---			ACTGGACTGGCTCGCTTGTGAGCCGGCTGAGCGGCTGGGACTGGGCTGACCACTCGCTCTTCAG AGACTGCCCGCGGTGACCACTGAGCTGCTGCC[C/G/A]GTGGGAAAGCAGAAAGCAGGACC
stSG4896	112 C T ---			AAACAAATCAAAACCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGTGGGGCTGGGCACCTTTTCT[C/T]CAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---			ACAGTGCCGATGGTTACACAA[T/G/A]TTGTAATGTATTTATCCCACTTACGAATGATTAATAATGA TAAATCTTATGTTTATTCATCACTACCAAAAGGCTGTGGTGCAAGGGTCTGGTTTCTGGTCT
stSG4950	24 A G ---			TCATGACTCCAGGAAAGGTCT[A/G]TCTTAGCTTCTCTCTCCCTACTTTCTCTACATGCTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---			AGATACGGGCAAAACACTGGGATGGCTTCCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGTT GGGAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCTAGGCC CC[G/A]GTGACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 C T ---			GAAGTGCTCTGAGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA[C/T]AGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---			ACTGGTGCCTCTCAGCAGATTGAGGGGTGTCAGGGGTGTTACCACAACTCAGTAGGAGTGCAA GGGCT[A/G]TACCCCGGAGCTAGACAGCCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTGTGTGC AACCTTG
stSG4997	22 T C ---			CAAAGGAGTAGGAGCCCCAA[T/C]TTTAAATGGTTTCTCTCCCTCATGCTATTGTATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAT
stSG6312	37 C T ---			ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAACA[C/T]TATGCCATCGGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---			GCTCTGGTCAAGCAAATTCCTCAGGACAGAGCAACAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC[G/A]ATAGTTCAAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTTGTCTCTTTGGCCTGTTGTGGACAGAAAGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG6362	88	G C	---	---	TGTGAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAAGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62	G T	---	---	CACATCTGTGTTTCTGGAGCAAGGGAACACAGAGGCCAGGAGTTTGGGTGTCACCTGG[G/T] GTCITTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAAGAAATAGA TGGCTT
stSG8022	53	G A	---	---	AGCTCCTGACTCCCTGTTCACTGACGTCACTGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAACTGGAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67	G C	---	---	TGATTGTTAGGGATAAGTGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAAATTGTGTGTT G/CTGGGAGGAGGTAGCAAGATAAAAGAGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C A	---	---	AGCTGGCTCTTCTTCTGTGCTGTTGGGAGGCTTACGTCTCTCG[C/A]CCGTGGTCCCTGGTGGCC TGCAGGACCAAGGGGTGGGAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8064 a	23	G C	---	---	AGCTGGCTCTTCTTCTGTGCTGTTGGGAGGCTTACGTCTCTCG[C/A]CCGTGGTCCCTGGTGGCC TGCAGGACCAAGGGGTGGGAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8072	59	A G	---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGTCTTGTCTTGTAGGG[A/G]TGGC AGAGGCAGAAAGGAAGTCCGAGTATTAGTGGCCGCATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40	A G	---	---	ATACACCCACACACCCCACTCAACCTTGATATCAAAATCCA[A/G]AAGTGTAAGTAAAGTATAAGAAAT ATCATGACTAGTTAAAGATAGCAAAATACCATAAGGTACAAAGTTCAAGTATTAGTATAACAAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138	T C	---	---	AAGGCTCCTTTGAAGCATGGTTTATTGTTCCATTAACTTGTCTCAGCTATACTGAAGTATGATT GACAAATAAAACTTGCATATAATTTGAGATGTACAGTGTATGATACATGTATGTATACAAATGTGAAA TGAT[C]TGTCAATAATCAATAATGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110	A G	---	---	CAGTGGTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGCTTGTAAATACACAGATGACTAGGCC CACCTGCGGAGTTCCGTGGAGTCTAGGCCCTGAGAAATATTC[A/G]TTTCTAACAAAGTTCCCAGGTGA CCCTGAGGCTCTTGGACTGGGAACATGCTTTGAG
stSG8130 b	96	T C	---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGGTCTTTTAAAGTTTCAAAAT GACATTCAGACAAAGCGGTGCTGAGCC[T/C]GTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36	C G	---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGA[C/G]TGGATGGTGGTCTTTTAAAGTTTCA AATTGACATTCCAGACAAGCGGTGCTGAGCCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124	T A	---	---	TTGTGGACTTCAAAATCTTTCCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATTTGTGAACACAAATCTAAGAAATGAATGAGATGTT[A]CTGAAA TCTGATTCAAACACTTATCTTAACTGACTTCTGTCAATCCTCTGCTGTGAAGG

stSG8145 a	97	C T	---	---	TTGTGGACTTCAAATTCCTTCCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAATTTGTGAAC/C/TJACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACTTATCTTAACTGACTTCTGTGCAATCCTCTGTCTGTGAAGG
stSG8150	36	A G	---	---	ATTGTTCTTGGCAATTGCTTGGATTTTTCAGAATAGT/A/GJATAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTTCTATGTTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAAT GGGAAAT
stSG8340	30	C T	---	---	AGAGGATTATGAGAGAGCTGGGCAGGATC/C/TJCAACATTATGACCCTGAACCTCCAGAACTGGAT TCACTAGAGAGAGAGAGAAACGCTCATCAAAA
stSG8466	111	G A	---	---	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACCTTGTTACAAGGTATTTGCACCTACCTJ[G/A]TGAAGCAGCACAGCATTTAT TTGAAAG
ESTD-ACE	--	--	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCGCTCCCTGCTGCTGGGGGCCAACCCCGCTTCCATGA GGCCATTGGGACGTGCTGGCGCTCTCGGCTCCACTCTGAAACATCTGCACAAAATCGGCTGC
ESTD-ADA	--	--	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCTGAGCTTCTGGGCTCTGAGTCTGTCTC
ESTD-AK- 168	--	--	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	---	AATCCAGCACCTTAGGAGGCTGAGGCAGGCATATACAGAGGTGAGGAGTTTGAGACCAGTCTGA CCAACATGTTGAAACCCCATCTCTACTAAAATAACAAATTAGCCAGGCATGTTGTGTCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCGAAGTTGTGGTGAGCCGAGAT GGCACCATTGCACTCCAGCTGGGCAACAAGAGTAAACTCTGTCTC
ESTD- ANT1	--	--	---	---	TCTCCTGTCTACTCTCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTGCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD- APOA2	--	--	---	---	CCAGGTGTTGTGGCACGTGCTGTATATCCAGCTACTCGGAGACTGAGGCATGAGAACTCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCAGGTGACAGAGCAAG ACTCC
ESTD- ARSB	--	--	---	---	GGAAGAAATGGAGCCTGTGGAAAGGAGGCGTCCGAGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCAAAC

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCCTCTTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGGAGCGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGTGGCCACC GTGGAGGGCAACCTGCTGTATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGAOCAAACGT GTTGCTGACTTCGCTGGCCGCGCAGCCGACCTGGTGTGATGGGACTCCTGTTGGTCCCGCGCGGCCACCTT GGGC
ESTD- BA511	--	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGTGCAG TGAGCCAAAGATGTGCCACTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTATAACTCCTCTCTTCTCTGGGGCCGTGGGTGGGAGCTGGGGCAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGTACGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGCAGAGGGCTACGAGTGGGATGCGGGAGATGTGG GCGCCGCGCCCCGGGGCGCCCCCGCACCGGCATCTTCTCCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTGAGAAACCCATAGAGCCCGGAGACTCATCTGCGCAAGA GACCAAAGAGGTGAGCTTCTGTGTCCCGGGAAGGAGGAGGAGGTGACAAAGCTAACTCTGCTTCAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGCGACA
ESTD- BRCA1a	--	--	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAAATGTAAAGAAAATCTGCTAGAGGAAACCTTTGAGGAACATTCAATGTACCTGAAAGAGAA ATGGGAAATGAGAAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCCCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCTCCTCCCTAATTTGCTCCGGGAAGCACATTCAACAA CCCAGTCAGTTTGGGGACAGCCATGCAGCTGAGCCTCTGTGTAGCCTTTCAACCATGCATTCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-C7	--	--	--	--	---	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAAACCATAGGGCGGATACAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCTTTCCGGCCTTCTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCGGCCTTCTCTCTCACACATACAGAGCCCTACCAGGACAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAA
ESTD-CB24	--	--	--	--	---	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGACCTGAA AAACGTGTTCCACCCGAGGTCGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCGACACAGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTCAGCACAGACCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	---	GTTTTCTTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTCTTTTCTCTCTATCTTTGCGCGTC TCTGCTCTCGAACCCAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	--	---	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTAGGTAAGCTAAACCAATAAAAAT TGTTGTTGGGCTGGTTGCAATTCAGGAGTGCTGTGGAGTTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTTCATCCTGATGGAACTCCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	---	AGAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTGTCACCTTTCAGGGTGTTCAGGTGGAAGGT GAACAGGGTCCCGTGGTCCCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	---	TGAGAGAACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACACTGGACTTCTTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	---	GCCGCAATGCCGGGAGTTTCTCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCCCTTAGAA GGCAATCCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAC TGGGAGGCCGGCATAGTGTCTCATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGGGGTGGATCAC TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTCATCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGIGTGAGIATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGCGTGGTCGAGGTGGTCAACCATCCCGCAGAGAACAGGTGAGCCACCCACTATGCACAGGT TCTCATCAATTGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACAATTTTAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTCCCAATTACTTGCAATCTAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAATATTACATATCTGGATTAAATTATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCGGTG GGGTTGTGTGGCTATGTGGTGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATTGCGTTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCAAACATGGGGAATCACATCTCTACCAAATTAACAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATTGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTGT TTATTCAAACTATTTATCACCTTATTTTATTGGTAAGCCATACATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTCTGATGTTTCCAGGAGCCTTGATGTCTCTCTCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTACAGCTGATTCCC AGAAGTGAACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGTATTT CTTAACAATAAATGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGATAAATGTTATTT TAGCTGTGAGAAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGATT GCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTTCATGCACTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCACGATAGGCTTTCTCTACTAATACAGAAATTTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGCAATCACTTCTTCTTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTTTTACAAAACATTTTCATCCATGGACTCCATCTAG AATATTTGAAGAAACAAACATGACAAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGCAOCTGTGGCTCAAGCAGCTGCTGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTATCTGTGGAGAACCAAGAACTTCTGGCCTGTGGTAGGGGAGCTGCTTCCAAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	--	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAAGATCCAAACCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGCCCTTTGTGTCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCAACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCCG TCCCACCAACGGTCTCCACAGCACTCCGACAGCCCGCCAAACCCAGAGAAAGATGGGATGCCAAAG ACCAACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTGAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCTGTGAGGAGAGA
ESTD- ERB82	--	--	--	---	---	TCTTTCAGGATCCGCATCTCGCCTGGTGGGCATCGCTCCGCTAGGTGTACGGGCTCCACAGCTGG GGTGAGGGGGTGGTGCTCAGTGCCGGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCACCC CGCTCACCTCCGTTTCTGACGAGCTCTCCGATCGTGTACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTGCCTTTAAGTGAAATGGTCGAGAAAGAGGCCACCGAGGAGCCGCTGGCGCCTGGCA GTCCGTGGACCGGATGTTCTGGCTGTTTGAATTTCTCAAAGGAGCGAGCATGTGCTGGACACACAC AGACTATTTTATGATTTCTTTTGGCTTTTGCAACCCAGGAAACAGCAATGCCAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAAACAAACCATGTCAITTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAAAGGCCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAC

ESTD- GODH	--	---	---	---	---	CGCAGACCGGTGAGTGTGGGTGGGAGTGTGGAGGGAAGGAGGGAAGGAACTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAAGCGGGGAGAAACACAGAGCCAACTGGCTAA GTGTAAGGGGACCTCTGGTCGCACOGTGTGTTCTGCTGCCCTGTTTTCAGCTGTCTGTCTGCCGAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	---	---	---	---	GTTTATGCAATGCGAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGGCCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	---	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACAGGCATCATTTG AAACCAAGTTTCCGTCAAAGACTTGAAATTCAGGTAAGTGATGTTCCCTAGG
ESTD- GPPK2L	--	---	---	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCCGCCGAGAACTGCTCGATAATC
ESTD- HRAS	--	---	---	---	---	CTGGGCTGCGCCGAGCAGCTGTCTGGCACTGGACGGGGCGCCAGGCTCACCTCTATAGTGGGTGCG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	---	---	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTGGCAATGTGGCCTGGGCCACATTTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCCGGCTCCGGCTTGATTCC AGATGGAGCTTTCCTTTATCCCTGATGTATGGATTGGCTTCCTGCTG
ESTD-HT2	--	---	---	---	---	GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGAAATAAAAGGATAACCTGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT4	--	---	---	---	---	ACCAACGAGCCGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCCCTTCTATCGGCAAGAAATGCGTACTTATTTGAATAGTAGAGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCCTAAA TGACAGCCGAAGAGGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	---	---	---	---	AACACACAAGCCCCAGCGAGAATTGAACTCGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGTGTTGGTTTCTTCCCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTCTCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	---	---	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCGAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTTATTTTITTTTG AGATGGAGTCTGGCTCTGTCAACCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTTCATGCCATTCTCCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCCTACCCCTCCCTTAGCCCGTGGGAGCAGGAAATCTCTCTCCAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCGTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTTGAGGCTCAGTTAATAATTTCAAATTTGTAACCGTAGCAAAACTGCATTGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGTGTTATACCTGCCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAGGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTCTGCCCTGTCTGCTGCCTGCA AGGGTTTGTCTTAATTCTCAATTCATGTCTCTTCACTCTTTTAGCAGCTGTGGGTTTTGTGTGTTTC TTCTGTTTTGTCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTTATAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG
ESTD- METH	--	--	--	---	---	CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTTCCAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTTCATG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCACAGACTGATATGGCTGGT

ESTD-NFKB1	--	--	--	---	---	---	AAATGACGCTTGTATATTTGTACAAAAAAGTTTTATTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGTGTACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGGACGAGAAAGATCATTTGAAATTTCTGAG AAAACCTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	--	--	--	---	---	---	TGTCCTAGGCCCCAGCCCTGCTTGTCTCCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD-NRAMP	--	--	--	---	---	---	GGAGGAGGAGGTGGGAGGGGCTGTCTGTCTCCAGGTCCACAGACACAGAGAGCGGCTCAGTG TATCCCCACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-NRAS	--	--	--	---	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGTTTTCTTTATGTAGGTGATATTGGATACCTTTTGTGTTGATTATATATTAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGTTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---	---	GTGACCTTCTCACCTTTAAAAAATTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAAACA
ESTD-PAI1	--	--	--	---	---	---	GCCACACCACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGAGTCAGCCGTGTATCATCGAGCGCGCGGCAC ATGGCAGGATGAGGGAAGAACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	---	CTCTCAGGAACCCAGCTCTTCTTACCAACACAGACTTATTGCTGCTCCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCC
ESTD-PBDA	--	--	--	---	---	---	CCTTCTCATGCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTCTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGTGCAACATTGAAAGCCCTCGTACC
ESTD-PS-1	--	--	--	---	---	---	GGGAGTAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACACCATAGCCTATTTCGTAGCCATATTAAATTTGTGCTTACATT ATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT CTACTTTGCCACAGATTATCTTGTAT
ESTD-PXMP1	--	--	--	---	---	---	ATGAAACATGGTCTTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAAGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
ESTD-Per/RDS	--	--	--	---	---	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAAGAGCGTGCCGAGACCTGGAAGGCCT

ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGGGGCTGGCTGGAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGCAACAGGTGAAGCCGAGGGCGCAGACGCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	CTTCGTGACGGGAGGTACGTCTCCGCTCTTTCTATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGATGAACAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAACTCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCAITGCTACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAAACACCCCTGTGGTCCGGAGCCAGGTGTGTCTCTCTGGAGCCCTGAGGAGTTGTGTGTGTG CAGTCCCCCGGCCACCTGTGTGTGAGCCTGGACATACACCTTCACCTCTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTGTGTGCACACCCCTCTGTGAAGACCCCAACCCCTGCCCTCC CCCACCCAAAGCCAGTTTCTAGCAAGGCGAGAC
ESTD- SSA1	--	--	--	---	---	TTCACTTTGTGGATTGTTCTTTGTGTGCGACGACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTCTGTGA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGCCCATCAGTTCATCAGCTC CCATGACTGGGATGCTAAGTCAGCACTGAGTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCCCTCTCACCTAGAACGTTTGTTTACAACCTTTCTTCCAGTATGGATGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	--	--	--	---	---	TGCGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAGAGAAAGAGTCCCAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCATTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTGGAGGGCATGAGGACGGGTTTCAAGCTCCAGGTCTTACACACAAATCAGTCAGTG GCCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCAACTTTCCAAATCCCGCCCGCGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGGATTCTTGTTCACCAGCAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTGTCTTCTGCGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATATTGATGTCGTGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGATGACA

ESTD- TYRP1	--	--	--	---	---	AGTAGTGATGAAGCTAACAGCCTCTCCTCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAACTCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACCTTTATTACCTTTCTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACCT
ESTD- VB12	--	--	--	---	---	TTCCCAAGGCCTCAATACAAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAAGGTACAGAGACAGGAACACCAGTG ACTCTGAGATGTCACAGACTGAGAACCCGTTTATATGTACTGTGATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCCTGCAGGATGIG CGACGTGTGCTGGAGTAGCCCGACTCTTGTACGGTCCGTCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACCC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGTCAAGCCTCAGCACCAGATGCTGTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGACAGAGAGTTATTTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCCTGACAGATACCAGCTGTTGGTGGAAAGG AGTGCCCACTGCCAGGCTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAAGTCAACCTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCACTCTATTTGCCAGCCCCAGGACAGAGCTGATCCTTGAACCTTAAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCCAAGACCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCCGAGAAGGAGGTGCTGCTGCTGCCCTGCCCG GTCACCTC
EST51976 7	--	--	--	---	---	AGGCAGAAACTGGGCCCCCATGGGGGACGTGGAGGCCACTTGAGCTTCTGGAGAGGACCTGA GGGACAAGGTCAACTCCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGAGGAGTGCAGATGCTGGCC CCTTGGAGAGCTGAGCTGCCCTGGTGC

EST11458 6	--	--	--	---	---	CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAAACATTTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCCTCCTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTGGGGCCCGTGG TCCTCCTGGTGTGGGTAGTCTGGAGTCAACGGTCTCTCTAGTGAAGCTGGTCTGATGGCAACC CTGGGAACGATGGTCCCAAGGTCGGATGGTCAACCCGACACAAGGAGAGCGGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAATGGTACCCAACTTGCCCTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTGATGATGATGAGGAGACTGGAAACCTGAAACAAAGG CTGTCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGATGATGGTCTCTAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTTCTTCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATATTCTTCCCTCTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCTCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAAGCCAGGCACTGGGCTCCGGAGGACTCAOCCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST44438 7	--	--	--	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCGCCTCAAGAGCCGAGCGGAGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGGTGGTACTTGAAGTAAGGAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGTTATTTGGGTTAGCGTGGTGTGATGTTGTCTACTA TAGTCCAAGTGAA

EST10398 2	--	--	--	--	---	---	TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTTACACATTTGGGGCTTGACCTTTCCAAACAGGAGAAG CATTGTTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCAATTTG
EST36751 7	--	--	--	--	---	---	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTTAACTCGATTACTTTTTCTATTCAAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	--	--	--	--	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAGAATCTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACTGGATGCATTATAACAAATATTTTACCCTTTGAAAAAATAAATG AAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTTGAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	--	--	--	--	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGTAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	--	---	---	TCCCGCCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCCACCCCGGCGACTCACCGCTCT CGCTCTCGGTAAACATCCGGCCGGCGGCTGCTTGGACACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCTCCGGGCTTGGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	--	--	--	--	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCCTAGAAAGATACACGAGACCGA ATGTATCAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAAACCTT
EST74167 6	--	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGGGGCAGGCTGTCCAAGGAGCTGCAGGGCGGCGAGGCCGGCTGGCGCGGACATGGAGGA CGTGGCGGCGCGCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGAGC TGCGGTGGCGCTCGCTCCACCTGCCAAGCTGCGTAAGCGGCTCTC
EST43211 8	--	--	--	--	---	---	CGCTGGTGCAGTACCGGGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCCGGATGCCGATGACCTGCAGAAAGCGCC TGGCAGTGTACAGGCGGGGCGCGGAGGGCGCGGAGCGGCGCTCAGCGGCATCGCGGAGCGGCTG GGGCGCTGGTGAACAGGGCGCGGTGCGGGCGCGGCGGCGGCTG
EST36770 4	--	--	--	--	---	---	TGTAGCCAAAGTCACTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCCAAAT TCAACCTCCCGATAGGGCTGGGCTTGACCAAAATATACTGGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAGGCCCTAAGAAAGGCTTATG

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTGGAACCTGT CCATAAAGTAATTTGTGAAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACCTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCCCTTTTGCAACAAGACAAAGCAAGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTTGAGCCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTCCGAATCCTCCTCCTGAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGGACGCGGCTCTCTGCGTGCATCCTAAGCTCT GAGAGCAAACTCCCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGCTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTCACACATTCAGAAGAGGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCCTATGGGATTTGACITTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGCACTCATGACAAATTTGAAGCTGACAATTACACAAGAAAGGAATAAATTCACAGTCAA AGAATCAAGCACITTTTCGAAACATTGAAGTTGTTTTTGAACCTTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCCCACAAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAGAGAAAGAGAACCCAGAAAT CACAGTGGGCACGTGCGTCTACCGCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	--	--	--	---	---	TCCAGGTGGCTGGACCCAGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCAAGGCAGGCACTGCGCTTCAGCCTGCTCAGCCCTGCTGTCAC CCAGATCACTGCTCTCTGCCATGGCCCTGTGGATGCGCCTCTCTGCCCTGCTGGCGCTGCTGGCCCTC TGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTCCAATTCTGTCCCTATAGTTTTCTCTATTAAGTGAACATACATGCACTTTTAGT GGATAGATGCACACAACACACAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST ID	Position	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
EST65258	8	---	---	---	---	---	---	---
EST38216	3	---	---	---	---	---	---	---
EST62782	2	---	---	---	---	---	---	---
EST35879	9	---	---	---	---	---	---	---
EST68308	5	---	---	---	---	---	---	---
EST54045	6	---	---	---	---	---	---	---
EST52908	0	---	---	---	---	---	---	---
EST19590	2	---	---	---	---	---	---	---
EST76136	2	---	---	---	---	---	---	---
EST58607	0	---	---	---	---	---	---	---

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.